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OM nucleic - nucleic search, using sw model

Run on: November 28, 2003, 15:41:35 ; Search time 8038 Seconds
(without alignments)
11527.761 Million cell updates/sec

Title: US-09-928-175-1

Perfect score: 2265
Sequence: 1 atgattgcttcttcgttctt.....taatgaaccagtttctctag 2265

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl.*
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4: gb_om.*
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8: gb_pl.*
9: gb_pr.*
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11: gb_sts.*
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13: gb_un.*
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38: em_by.*
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40: em_hugo_mus.*
41: em_hugo_other.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2265	100.0	2265	6	AX385027	AX385027 Sequence
2	2265	100.0	2838	9	AF403384	AF403384 Homo sapi
3	2261.8	99.9	2436	9	AF453828	AF453828 Homo sapi
4	2258.8	99.7	2262	6	BD141180	BD141180 Novel G p
5	2214	97.7	2214	6	AX451562	AX451562 Sequence
6	2111	93.2	2193	6	AX385032	AX385032 Sequence
7	2104.8	92.9	2190	6	BD141181	BD141181 Novel G p
8	2060	90.9	2142	6	AX451566	AX451566 Sequence
9	2002.2	88.4	2181	6	AX709190	AX709190 Sequence
10	1803	79.6	2049	6	AX385037	AX385037 Sequence
11	1579.8	69.7	2539	10	AF346501	AF346501 Mus muscu
12	1579	69.7	2214	6	AX385045	AX385045 Sequence
13	1543.4	68.1	1545	6	BD141175	BD141175 Novel G p
14	1389.4	61.3	1473	6	BD141176	BD141176 Novel G p
15	1384.8	61.1	1830	6	BD141172	BD141172 Novel G p
16	1149	50.7	1149	6	AX385030	AX385030 Sequence
17	1066.4	47.1	1068	6	AX148176	AX148176 Sequence
18	1065	47.0	1065	6	BD141178	BD141178 Novel G p
19	995	43.9	1077	6	AX385035	AX385035 Sequence
20	991	43.8	1101	6	AX385042	AX385042 Sequence
21	825.8	36.5	1140	6	AX385048	AX385048 Sequence
22	735	32.5	1274	6	AX349337	AX349337 Sequence
23	735	32.5	2274	6	AF190500	AF190500 Homo sapi
24	735	32.5	2467	6	BD135245	BD135245 Novel mam
25	687	30.3	933	6	AX385040	AX385040 Sequence
26	686.2	30.3	3584	6	BD135246	BD135246 Novel mam
27	566.6	25.0	653	4	AX196483	AX196483 Equus cab
28	547	24.2	575	6	AX356204	AX356204 Sequence
29	482.2	21.3	1191	6	AX128507	AX128507 Sequence
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36	280.2	12.4	211251	2	AC121029	AC121029 Rattus no
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38	280.2	12.4	239190	2	AC098990	AC098990 Rattus no
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ALIGNMENTS

RESULT 1
AX385027
LOCUS
DEFINITION
Sequence 1 from Patent WO0214489.
AX385027
VERSION
AX385027.1 GI:19578152
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
AUTHORS
TITLE
Paszy, C.J., Gong, J., Daugherty, B. and Rogers, N.
Leucine-rich repeat-containing g-protein coupled receptor-8
molecules and uses thereof

Pred. No. is the number of results predicted by chance to have a

JOURNAL Patent: WO 0214489-A 1 21-FEB-2002;
Amgen, Inc. (US)
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FLSCSLTVLFLPRNIGFVPEKPESSKANGEDLSNITTELSPLFKDLKLOK
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sig peptide 1..108
BASE COUNT 650 a 466 c 423 g 726 t
ORIGIN

Query Match 100.0%; Score 2265; DB 6; Length 2265;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2265; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
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DEFINITION AF40384
ACCESSION AF40384
VERSION AF40384.2 GI:18702459
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2838)
AUTHORS Hsu, S.Y., Nakabayashi, K., Nishi, S., Kumagai, J., Kudo, M.,
Sherwood, O.D., and Hsueh, A.J.
TITLE Activation of orphan receptors by the hormone relaxin
JOURNAL Science 295 (5555), 671-674 (2002)
MEDLINE 21669315
PUBMED 11809971
REFERENCE 2 (bases 1 to 2838)
AUTHORS Hsu, S.Y., Nakabayashi, K., and Bhalila, A.
TITLE Direct Submission
JOURNAL Submitted (26-JUL-2001) GYN/OB, Stanford University, MSOB S385,
Stanford, CA 94305, USA
REFERENCE 3 (bases 1 to 2838)
AUTHORS Hsueh, A.J. M.
TITLE Direct Submission
JOURNAL Submitted (19-FEB-2002) Division of Reproductive Biology,
Department of Gynecology and Obstetrics, Stanford University
Medical Center, 300 Pasteur Drive, Room A-344, Stanford, CA
94305-5317, USA
REMARK Sequence update by submitter
COMMENT On Feb 19, 2002 this sequence version replaced gi:18419431.

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Matches 2265; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 3
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 descent (GRBAT) mRNA, complete cds.
 AF453828
 AF453828.1 GI:18483167
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
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 Homo sapiens
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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 1 (bases 1 to 2436)
 Gorlov, I.P., Kamat, A., Bogatcheva, N.V., Jones, B., Lamb, D.J.,
 Truong, A., Bishop, C.B., McElreavey, K. and Agoulnik, A.I.
 Mutations of the GREX1 gene cause cryptorchidism
 Hum. Mol. Genet. 11 (19), 2309-2318 (2002)
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 REFERENCE
 Agoulnik, A.I.
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 Submitted (30-NOV-2001) Ob/Gyn, Baylor College of Medicine, 6550
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LOCUS BD141180 2262 bp DNA linear PAT 18-SEP-2002
DEFINITION Novel G protein-coupled receptor protein and its DNA.
ACCESSION BD141180.1 GI:23236125
VERSION BD141180.1 GI:23236125
KEYWORDS WO 0204640-A/9.
SOURCE Homo sapiens (human)
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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2262)
AUTHORS Moriya,T., Ito,T., Shintani,Y. and Miyajima,N.
TITLE Novel G protein-coupled receptor protein and its DNA
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PD 07-JUL-2001 WO 2001JP005878
PR 07-JUL-2000 JP 00P 211989,18-DEC-2000 JP 00P 383794 PI
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CC Novel G protein-coupled receptor protein and its DNA. FH Key

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 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 1
 Feder, J.N., Mintier, G., Ramanathan, C.S., and Hawken, D.R.
 A novel human g-protein coupled receptor, hgrp5, expressed
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 Patent: WO 0226824-A 1 04-Apr-2002;
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 VERSION AX385032.1 GI:19578156
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 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 1 Paszty,C.J., Gong,J., Daugherty,B. and Rogers,N.
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 JOURNAL Amgen, Inc. (US)
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sig_peptide 1.108
BASE COUNT 626 a 456 c 411 g 700 t
ORIGIN

Query Match 93.2%; Score 2111; DB 6; Length 2193;
Best Local Similarity 96.8%; Pred. No. 0;
Matches 2193; Conservative 0; Mismatches 0; Indels 72; Gaps 1;

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RESULT 7
BD141181 2190 bp DNA linear PAR 18-SEP-2002

LOCUS BD141181
DEFINITION Novel G protein-coupled receptor protein and its DNA.
ACCESSION BD141181
VERSION 1
KEYWORDS NO 0204640-A/10.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 2190)
Moriya,T., Ito,T., Shintani,Y. and Miyajima,N.
Novel G protein-coupled receptor protein and its DNA
Patent: WO 0204640-A 10 17-JAN-2002;
TAKEDA CHEMICAL INDUSTRIES LTD, TAKEDA MORIYA, TAKASHI ITO, YASUSHI SHINTANI, NOBUYUKI MIYAJIMA

JOURNAL SHINTANI, NOBUYUKI MIYAJIMA
OS Homo sapiens (human)
COMMENT PN WO 0204640-A/10

PD 17-JAN-2002
PF 06-JUL-2001 WO 2001JP005878
PR 07-JUL-2000 JP 00P 211989,18-DEC-2000 JP 00P 383794 PI
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PC A61P35/00, A61P37/00, G01N33/15, G01N33/50, G01N33/53, G01N33/566//
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CC Novel G protein-coupled receptor protein and its DNA. FH Key

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Qy 421 TTAAGTCTCTTAAAGAAACCAAAATCCAGTCTTCCAGATTAAGTTTCTCAATATAC 480

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DEFINITION	Sequence 5 from Patent WO0226824.						
ACCESSION	AX451566						
VERSION	AX451566.1	GI:21698550					
KEYWORDS	.						
SOURCE	Homo sapiens (human)						
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.						
REFERENCE	Feder,J.N., Muntzer,G., Ramanathan,C.S. and Hawken,D.R. 1 A novel human G-protein coupled receptor, hgrtm5, expressed highly in brain and ovarian tissues Patent: WO 0226824-A 5 04-APR-2002; Bristol-Myers Squibb Company (US) Location/Qualifiers 1..2142 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606"						
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 LOCUS Sequence 49 from Patent WO02063004.
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 ACCESSION AX709190
 VERSION AX709190.1 GI:29564784
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 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 1. Baughn, M.R., Tribouley, C.M., Nguyen, D.B., Thornton, M., Yao, M.G., Kallick, D.A., Gandhi, A.R., Walla, N.K., Arvizu, C., Elliott, V.S., Hafalla, A.V., Ramkumar, J., Pel, J., Tang, Y.T., Ye, H., Reddy, R., Burford, N., Lu, D.A., Graul, R.C., Khan, F.A., Walsh, R.T., Ison, C.H., Richardson, T.W., Griffin, J.A., Warren, B.A., Yang, J., Lee, E.A. and Harland, L.
 G-protein coupled receptors
 Patent: WO 02063004-A 49 15-AUG-2002;
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 AX385037
 AX385037
 AX385037.1 GI:19578160
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 ORGANISM
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 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 Pasty, C.J., Gong, J., Daugherty, B. and Rogers, N.
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Db		1465	GATTATTTTGGAAACTTTTATGGGAAAAATGGAGTAGTGTTCCTCCACTTATATGACCAA	1524
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ACCESSION		AF346501		
VERSION		AF346501.1	GI:15811372	
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SOURCE		Mus musculus (house mouse)		
ORGANISM		Mus musculus		
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		Overbeek P.A., Gorlov I.P., Sutherland R.W., Houston J.B.,		
		Harrison W.R., Boettger-Tong H.L., Bishop C.E. and Agoulnik A.I.		
TITLE		A transgenic insertion causing cryptorchidism in mice		

JOURNAL	Genesis 30 (1), 26-35 (2001)
MEDLINE	21250590
PUBMED	11353515
REFERENCE	2 (bases 1 to 2539)
AUTHORS	Agoulnik, A.I.
TITLE	Direct Submission
JOURNAL	Submitted (06-FEB-2001) Db/Gym, Baylor College of Medicine, 6550 Fannin Str. Su. 861, Houston, TX 77030, USA
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RESULT 12
 AX385045
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 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Mus musculus (house mouse)
 Mus musculus
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 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE
 1 Paezzy, C.J., Gong, J., Daugherty, B. and Rogers, N.
 Leucine-rich repeat-containing 9-protein coupled receptor-8
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 Patent: WO 0214489-A 19 21-FEB-2002;
 Amgen, Inc. (US)
 JOURNAL
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BASE COUNT
ORIGIN

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Matches 1823; Conservative 0; Mismatches 385; Indels 3; Gaps 1;

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232 AACAGGTGGCTTAAACAGAGAGTCTTTTAAACAGTATCCAAATGCTGTGATGTC 351
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352 AAAAGAACTGAATTTGAAATGTGTAATGCTTAAAGTCTGTGCGGATGATTTCTAAC 411
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481 AGGAGAGCAATCTTGGATTATGTAATGCAAAATCTGATCTGACCATTAAGTCAAT 540
592 ACAACCTTCAGACTGGAATATTTCAAGACTTAACATCACTTAAGTCTTAATTTAGAT 651
541 AACTCTCTCAGGCTGGGATATTTCAAGACTTGCATCACTTGGCTTAATTTAGAT 600
652 GACATTCACATTAACAGAAATTTCAAGGCTGTTTACGAGATTAATTTCTTGTGTTTC 711
601 GACAAACCCGATACACAGAAATTTCAAGAGTCTTATAGGGGTAAACTCTTGTGTTTC 660
712 CTGTATAGGTTAATTAATTAAGAGTCTTCCAAAGATGATGATGATGATGATGATGAT 771

Db 661 TTGTTCATGATGGGTAACCGGCTCGAGCCCTTCTCTGAACATTTGTGCTCAGATGCT 720
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Qy 1012 TCCAACTCTTATGATCTTCAAGAAACAGTTTGAAGTCTTAAACAACTTCACT 1071
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Query Match	68.1%	Score 1543.4	DB 6	Length 1545
Best Local Similarity	99.9%	Pfed. No. 0		

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QY	1498	TTTCTGCGCAATGCTGTCCACGAGTCTCTGTTCTGTACTGACCTTACTTGAATCTTTGGAG	1557
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1918 TTCTTTTATAGTGTCTGATGCGCATCTGCGGATTCCTGTATTTGTTGTTAAATC 1977
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RESULT 14

LOCUS BD141176 1473 bp DNA linear PAT 18-SEP-2002
DEFINITION Novel G protein-coupled receptor protein and its DNA.
ACCESSION BD141176.1 GI:23236121
VERSION WO 0204640-A/5.
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1473)
AUTHORS Moriya,T., Ito,T., Shintani,Y. and Miyajima,N.
TITLE Novel G protein-coupled receptor protein and its DNA
JOURNAL Takeda Chemical Industries Ltd, Takeo Moriya, Takashi Ito, Yasushi
Shintani, Nobuyuki Miyajima
COMMENT OS Homo sapiens (human)
PN WO 0204640-A/5
PD 17-JAN-2002
PF 06-JUL-2001 WO 2001JP005878
PR 07-JUL-2000 JP 00P 211989, 18-DEC-2000 JP 00P 383794 PI
TAKEO MORIYA, TAKASHI ITO, YASUSHI SHINTANI, NOBUYUKI MIYAJIMA PC
C12N15/12, C12N1/21, C07K14/705, C07K16/28, C12P21/02, C12Q1/68, PC
A61K38/00
PC A61K45/00, A61K48/00, A61P1/00, A61P3/00, A61P9/00, A61P25/28, PC
A61P29/00
PC A61P35/00, A61P37/00, G01N33/15, G01N33/50, G01N33/53, G01N33/566//
PC (C12N1/21, C12R1:19), (C12P21/02, C12R1:19)
CC Novel G protein-coupled receptor protein and its DNA. FH Key
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BASE COUNT 405 a 310 c 278 g 480 t

ORIGIN

Query Match 51.3%; Score 1389.4; DB 6; Length 1473;
Best Local Similarity 95.3%; Pred. No. 0;
Matches 1472; Conservative 0; Mismatches 1; Indels 72; Gaps 1;

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1 ATGGTATATACTACTAGAGAGCTCTCCAGAGAGATGTGTGCCAAATGCCCAATC 60
778 AACTGGGTGATTTGGAGGCAATAGATTAAGTATCTCAAAATTTAGCTTCTGTG 837
61 AACTGGGTGATTTGGAGGCAATAGATTAAGTATCTCAAAATTTAGCTTCTGTG 120
838 TGGGATTTGGTCAAGAGCTGTTTCTGCTAGAAATCAAAATTTGTTTCCAGAGAG 897
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898 ACATTTTCTTCATTAATAAAATTTAGAGAACTGGATCTGTCTAGCAATAGATACGAG 957
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Search completed: November 28, 2003, 18:06:00
Job time : 8055 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 28, 2003, 15:41:35 ; Search time 582 Seconds
(without alignments)
10505.545 Million cell updates/sec

Title: US-09-928-175-1

Perfect score: 2265

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Scoring table:

IDENTITY NUC
Gapox 10.0, Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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3	2214	97.7	2214	24	ABK51944
4	2104.8	92.9	2190	24	ABL40197
5	2060	90.9	2142	24	ABK51947
6	2002.2	88.4	2181	24	AAF86580
7	1543.4	68.1	1545	24	ABL40191
8	1389.4	61.3	1473	24	ABL40192

9	1384.8	61.1	1830	24	ABL40188	Human G protein-co
10	1105.8	48.8	1121	25	ABT33349	NOVX DNA sequence
11	1065.4	47.1	1068	22	AA507943	Human G protein-co
12	1065	47.0	1065	24	ABL40194	Human G protein-co
13	735	32.5	2274	25	ABK24570	Human G protein-co
14	735	32.5	2467	20	AA225345	Human LGR7 long fo
15	686.2	30.3	3584	20	AA225346	Human LGR7 short f
16	547	24.2	575	24	AA205498	Human FSH-like GPC
17	496.8	21.9	1804	21	AA290524	Human G-protein
18	496.8	21.9	1804	24	ABX73054	Human G-protein co
19	482.2	21.3	1191	22	AA06507	Human G-protein co
20	411	18.1	429	24	AA598139	Human DNA for pote
21	370	16.3	592	22	AA546861	Human G protein-co
22	370	16.3	592	24	ABK61639	CDNA encoding nove
23	321	14.2	321	24	AA02027	Human novel G-prot
24	266.4	11.8	760	22	AA135687	Human musculoskele
25	266.4	11.8	760	25	ABX58675	CDNA encoding nove
26	232.4	10.3	576	22	AA546918	Human G protein-co
27	232.4	10.3	576	24	ABK61696	CDNA encoding nove
28	227.6	10.0	1126	25	ACA04807	CDNA encoding huma
29	226.4	10.0	572	24	AB190585	Human polynucleoti
30	222	9.8	612	24	ABX73081	Human GPCR CDNA #4
31	221	9.8	1018	22	AAH51001	Human nGPCR57 codi
32	221	9.8	1018	24	ABX70234	DNA encoding human
33	185	8.2	562	24	ABX73082	Human GPCR CDNA #4
34	184.4	8.1	530	22	AA195584	Human expressed po
35	184.4	8.1	530	22	AA135644	Human musculoskele
36	184.4	8.1	530	22	ABA06471	Human CDNA SEQ ID
37	184.4	8.1	530	22	AA528950	CDNA encoding for
38	184.4	8.1	530	22	AA528953	Human endocrine po
39	184.4	8.1	530	22	AA530187	DNA encoding rena
40	184.4	8.1	530	22	AA530845	CDNA encoding nove
41	184.4	8.1	530	23	ABK43875	DNA encoding novel
42	184.4	8.1	530	24	ABK83808	Human polynucleoti
43	184.4	8.1	530	24	ABT07785	Novel human nuclei
44	184.4	8.1	530	25	ABX58632	CDNA encoding nove
45	183.2	8.1	1089	22	AA199557	Human expressed po

ALIGNMENTS

RESULT 1	AA151335	standard; DNA; 2339 BP.
ID	AA151335	
AC	AA151335;	
XX		
DT	20-MAR-2003	(first entry)
XX		
DE	Human LGR9 G-protein coupled receptor (GPCR) coding sequence.	
XX		
KW	Human; gene; ds; gene therapy; LGR9; G-protein coupled receptor; GPCR;	
KW	muscle mass decrease; muscle atrophy; cryptorchidism; inflammation;	
KW	asthma; allergy; oedema; high blood pressure; low blood pressure.	
XX		
OS	Homo sapiens.	
XX		
FT	Key	Location/Qualifiers
FT	CDS	71..2335
FT		/tag= a
FT		/product= "Human LGR9 G-protein coupled receptor (GPCR)"
XX		
PN	MO2002102992-A2.	
XX		
PD	27-DEC-2002.	
XX		
PF	19-JUN-2002; 2002WO-US19528.	
XX		
PR	19-JUN-2001; 2001US-299385P.	
XX		
XX	(REGE-) REGENERON PHARM INC.	
XX		

PI Murphy AJ, Glass DJ;
XX WPI; 2003-157041/15.
DR P-PSDB; AAO16303.
XX
PT New human LGR9 G-protein coupled receptor (GPCR) polypeptide, useful
PT for treating or diagnosing disorders associated with altered LGR9 GPCR
PT expression, e.g. muscle atrophy, cryptorchidism or inflammation, and in
PT pharmacogenomics
XX
PS Disclosure; Fig 1A-F; 131bp; English.
XX
CC The invention comprises the amino acid and coding sequence of the human
CC LGR9 G-protein coupled receptor (GPCR). The human LGR9 GPCR is useful in
CC diagnosing and treating conditions associated with a decrease in muscle
CC mass or atrophy. The human LGR9 GPCR DNA and protein sequences of the
CC invention are useful for treating diseases associated with altered human
CC LGR9 GPCR expression, such as: cryptorchidism; asthma; inflammation;
CC allergy; oedema; and high or low blood pressure. The present DNA sequence
CC encodes the human LGR9 GPCR of the invention.
XX
SQ Sequence 2339 BP; 676 A; 482 C; 435 G; 746 T; 0 other;
Query Match 100.0%; Score 2265; DB 25; Length 2339;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2265; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGATGTTTTCGTTGTTTAAACATCTCTTCAGCTCAGATTGATTACATGTTCTT 60
DB 71 ATGATGTTTTCGTTGTTTAAACATCTCTTCAGCTCAGATTGATTACATGTTCTT 130
QY 61 CTACTTCATTTCATCGTTCTGATCAATGTCAGAGATTTTGACACTGACCTCAAGTAGATG 120
DB 131 CTACTTCATTTCATCGTTCTGATCAATGTCAGAGATTTTGACACTGACCTCAAGTAGATG 190
QY 121 ATCACTCTTCAGTCCAAAAGATATTTTCCCTGTGGGAATCTTACCAAGTCTTACC 180
DB 191 ATCACTCTTCAGTCCAAAAGATATTTTCCCTGTGGGAATCTTACCAAGTCTTACC 250
QY 181 CGAGCTTTTCACTGTGATGGCAGATGACTGTGGGAACGGGGCGGAGCAAGAGAACTGT 240
DB 251 CGAGCTTTTCACTGTGATGGCAGATGACTGTGGGAACGGGGCGGAGCAAGAGAACTGT 310
QY 241 GGTACACTAGTGAATGGGCGACATATTTGGCAAGTGCATGGAATGCTAACAGGCTG 300
DB 311 GGTACACTAGTGAATGGGCGACATATTTGGCAAGTGCATGGAATGCTAACAGGCTG 370
QY 301 GCCTTAAACAGAGAGTCTTCTTAAACAGATATCCAAATGCTGTGACTGCAAGAACT 360
DB 371 GCCTTAAACAGAGAGTCTTCTTAAACAGATATCCAAATGCTGTGACTGCAAGAACT 430
QY 431 GAAATGGAAATGTGTAATGTGACTTAAAGTCTGTGCGGATGATTCTTAACAATGTGACA 420
DB 431 GAAATGGAAATGTGTAATGTGACTTAAAGTCTGTGCGGATGATTCTTAACAATGTGACA 490
QY 421 TTAATGCTCTCTTAAAGAAAACAAAATCCAGAGTCTTCCAGATTAAGTTTATGAAATAC 480
DB 491 TTAATGCTCTCTTAAAGAAAACAAAATCCAGAGTCTTCCAGATTAAGTTTATGAAATAC 550
QY 481 ACAAAACCTTAAAGATATTTCTTCAAGATATGATTAAGACATATCCAGGAAAGCA 540
DB 551 ACAAAACCTTAAAGATATTTCTTCAAGATATGATTAAGACATATCCAGGAAAGCA 610
QY 541 TTTTGGATTAATGTAATCTGCAAAATTAATATCTCAACCAACCACTGATCAACCTTC 600
DB 611 TTTTGGATTAATGTAATCTGCAAAATTAATATCTCAACCAACCACTGATCAACCTTC 670
QY 601 AGACCTGGAATATCAAGACTTACATGAGCTTAAGCTTAATTTCTAGATGACAAATCA 660
DB 671 AGACCTGGAATATCAAGACTTACATGAGCTTAAGCTTAATTTCTAGATGACAAATCA 730
QY 661 ATTAACAGAAATTTCAACAGCGCTTGTGTTACGGGATTAATTCCTGTGTTTCTGTATG 720

DB 731 ATTAACAGAAATTTCAACAGCGCTTGTGTTACGGGATTAATTCCTGTGTTTCTGTATG 790
QY 721 GTTAAATTAATCTTGAAGCTCTTCCCAAGAGATGTGTGCCAAATGCTCACTCAAC 780
DB 791 GTTAAATTAATCTTGAAGCTCTTCCCAAGAGATGTGTGCCAAATGCTCACTCAAC 850
QY 781 TGGGTGATTTTGAAGGCAATGAAATTAAGTATCTCAAAATTTCAACGTTTCTGTCTG 840
DB 851 TGGGTGATTTTGAAGGCAATGAAATTAAGTATCTCAAAATTTCAACGTTTCTGTCTG 910
QY 841 GATTCGCTCAGAGTGTGTTCTGCTAGAAATCAAAATGTTTGTCTCAGAGAGACA 900
DB 911 GATTCGCTCAGAGTGTGTTCTGCTAGAAATCAAAATGTTTGTCTCAGAGAGACA 970
QY 901 TTTTCTTCATTAATAAATTTAGAGAACTGATCTGTCTAGCAATACGATTAACGAGCTA 960
DB 971 TTTTCTTCATTAATAAATTTAGAGAACTGATCTGTCTAGCAATACGATTAACGAGCTA 1030
QY 961 TCACCTCAGCTTTTAAAGACTTGAAGCTTCTACAAAACCTGAACCTGTCAATCCAT 1020
DB 1031 TCACCTCAGCTTTTAAAGACTTGAAGCTTCTACAAAACCTGAACCTGTCAATCCAT 1090
QY 1021 CTTATGATCTTCAACAAGAACAGTTGAAAGTCTTAAACAATTCAGTCTAGACCTG 1080
DB 1091 CTTATGATCTTCAACAAGAACAGTTGAAAGTCTTAAACAATTCAGTCTAGACCTG 1150
QY 1081 GAAAGATAGAGATTCCAATATTAACACAGATTTTCAACCCATGAGAAATCTTTCT 1140
DB 1151 GAAAGATAGAGATTCCAATATTAACACAGATTTTCAACCCATGAGAAATCTTTCT 1210
QY 1141 CACATTTATTTCAAAAACCTTGGATCTGCTCTATGCTCCCAATGCGGAATATGATG 1200
DB 1211 CACATTTATTTCAAAAACCTTGGATCTGCTCTATGCTCCCAATGCGGAATATGATG 1270
QY 1201 CCCTTACGAGACGGCATTTCTTCATTTGAGAACCTTGTGCTTAACAATATCTCAGAAAT 1260
DB 1271 CCCTTACGAGACGGCATTTCTTCATTTGAGAACCTTGTGCTTAACAATATCTCAGAAAT 1330
QY 1261 TTTGTCTGGGTATTAAGCTTCAATACCTGTTTGAATCTTTTGTCTATGCGATGAGA 1320
DB 1331 TTTGTCTGGGTATTAAGCTTCAATACCTGTTTGAATCTTTTGTCTATGCGATGAGA 1390
QY 1321 TCTTCAATTAAGCTGAAAATACAACTACAGCTATGCTCAAAATCTTTGTGTGCT 1380
DB 1391 TCTTCAATTAAGCTGAAAATACAACTACAGCTATGCTCAAAATCTTTGTGTGCT 1450
QY 1381 GATTCGCTGATGGGTGTTTACTTGTCTTGTGGAATTTTCAATTAATAACCGAGGG 1440
DB 1451 GATTCGCTGATGGGTGTTTACTTGTCTTGTGGAATTTTCAATTAATAACCGAGGG 1510
QY 1441 CAGTATCAGAAATATGCTTGTGCTGTGATGGAAGGCTGAGTCCGCTCATGGGGTTC 1500
DB 1511 CAGTATCAGAAATATGCTTGTGCTGTGATGGAAGGCTGAGTCCGCTCATGGGGTTC 1570
QY 1501 CTGGCCATGCTGTCCACCGAAGCTCTGTCTGTCTACTGACTTAATTGAGAGAG 1560
DB 1571 CTGGCCATGCTGTCCACCGAAGCTCTGTCTGTCTACTGACTTAATTGAGAGAG 1630
QY 1561 TTCCTGTGATGTCTTCCCTTCAAGTACATTCGACTGAAAACGGCAGACCTCATGTC 1620
DB 1631 TTCCTGTGATGTCTTCCCTTCAAGTACATTCGACTGAAAACGGCAGACCTCATGTC 1690
QY 1621 ATCTCTATTTGCAATCTGGAATGGGGGATTTTAAATAGCTGTAATTCATTTTGAATAG 1680
DB 1691 ATCTCTATTTGCAATCTGGAATGGGGGATTTTAAATAGCTGTAATTCATTTTGAATAG 1750
QY 1681 GATTATTTTGAACCTTTTATGAGAAAATGAGATATGTTTCCACTTAATTAATGACAA 1740
DB 1751 GATTATTTTGAACCTTTTATGAGAAAATGAGATATGTTTCCACTTAATTAATGACAA 1810
QY 1741 ACAGAGATATTTGAGAACAAAGGATATCTCTTGAATTTTCTAGATGTGAATCTGCTG 1800
DB 1811 ACAGAGATATTTGAGAACAAAGGATATCTCTTGAATTTTCTAGATGTGAATCTGCTG 1870

QY	1801	GCCTTTCCGACATCTGAGTTTCCGATATACATCTCTGTCATCTCAAAAAACGCGC	1866
Db	1871	GCTTTTCCGATCATCTGATGTTTTCCATATACATATGTTCTGTTCCATTTCAAAAAACGCGC	1930
QY	1861	TTGCAGACCAAGAGATGAGAAATGTTTTGGAAAGAGAGTGCGCTGTGTGCAAAATGCTTC	1920
Db	1931	TTGCAGACCAAGAGATGAGAAATGTTTTGGAAAGAGAGTGCGCTGTGTGCAAAATGCTTTC	1990
QY	1921	TTTTTTATAGTGTTCTCTGATGCAATCTGCTGGATTCCTGTATTTGTATGTTAAATCCTT	1980
Db	1991	TTTTTTATAGTGTTCTCTGATGCAATCTGCTGGATTCCTGTATTTGTATGTTAAATCCTT	2050
QY	1981	TCCCTCTTCGGGGTGGAAATACAGACACAAATGACTTCGAGATGATTTTTTTCCTT	2040
Db	2051	TCCCTCTTCGGGGTGGAAATACAGACACAAATGACTTCCTGGATGATTTTTTTCCTT	2110
QY	2041	CCAGTTAACATGCTTTGGAATTCGAATCCTCTATACTCTCACACCAACTTTTTTAAGAC	2100
Db	2111	CCAGTTAACATGCTTTGGAATTCGAATCCTCTCTATCTCTCACACCAACTTTTTTAAGAC	2170
QY	2101	AAGTTGAAAACAGCTGCTGCACAAAACATCAGAGAAATCAATTTTCAAAATTTAAAAAAA	2160
Db	2171	AAGTTGAAAACAGCTGCTGCACAAAACATCAGAGAAATCAATTTTCAAAATTTAAAAAAA	2230
QY	2161	AGTTTATCTACATCCATTTGTGTGATAGAGACTCTCTTCCCTGAAACTTGGGGTTTTG	2220
Db	2231	AGTTTATCTACATCCATTTGTGTGATAGAGACTCTCTTCCCTGAAACTTGGGGTTTTG	2290
QY	2221	AACAAAATPACACTTGGAGACAGTATTAATGAAACAGTTTCTAG	2265
Db	2291	AACAAAATPACACTTGGAGACAGTATTAATGAAACAGTTTCTAG	2335

Accession	Gene	Protein	Location/Qualifiers
ABL40196	ABL40196	standard; cDNA; 2262 BP.	
ABL40196	ABL40196	23-MAY-2002 (first entry)	
Human G protein-coupled receptor TGR17-5	Human G protein-coupled receptor TGR17-5	encoding cDNA SEQ ID NO:14.	
Human; G protein-coupled receptor; TGR17-5; nootropic; antiinflammatory; vasotrophic; immunomodulator; cyostatic; gene therapy; protein therapy; neurological; inflammatory; circulatory; degenerative; immune system; digestive disease; cancer; gene; ss.			
Homo sapiens.			
Key			location/Qualifiers
CDS			1..2262
			/tag=a
			/partial
			/product= "TGR17-5"
			/note= "no stop codon given"
MO200204640-A1.			
17-JAN-2002.			
06-JUL-2001; 2001WO-JP05878.			
07-JUL-2000; 2000JP-0211989.			
18-DEC-2000; 2000JP-0383794.			
(TAKE) TAKEDA CHEM IND LTD.			
Moriya T, Ito T, Shintani Y, Miyajima N;			
WPI; 2002-179706/23.			
P-Psdb; ABB06254.			

Pt	G-protein coupled receptor protein TGR17 of human origin and DNA
Pt	encoding it for diagnosis and treatment of cancer and circulatory and
Pt	other diseases associated with its expression -
Xx	
Pt	Claim 7; Page 130-131; 145pp; Japanese.
Pt	
Pt	The present invention describes a human guanine nucleotide binding
Pt	protein (G protein) coupled receptor protein designated TGR17, which has
Pt	5 variant forms (TGR17-1 to TGR17-5) of the receptor protein having
Pt	additional residues at the N-terminal. The TGR17 proteins have nootropic,
Pt	antiinflammatory, vasotropic, immunomodulator and cytostatic activities.
Pt	The TGR17 polynucleotides and protein can be used in gene therapy and
Pt	protein therapy. G-protein coupled receptor proteins are cell membrane
Pt	proteins mediating the cellular response to a large variety of signalling
Pt	molecules. The TGR17 polynucleotides and proteins can be used in the
Pt	diagnosis, treatment and prevention of diseases including neurological,
Pt	inflammatory, circulatory, degenerative, immune system and digestive
Pt	diseases and cancer. The present sequence encodes human TGR17-5 from the
Pt	present invention.
SQ	
SQ	Sequence 2262 BP; 650 A; 467 C; 421 G; 724 T; 0 other;
Query Match	99.7%; Score 2258.8; DB 24; Length 2262;
Best Local Similarity	99.9%; Pred. No. 0;
Matches 2260; Conservativity	0; Mismatches 2; Indels 0; Gaps 0;
Oy	1 ATGATGTGTTTCCTCGTTTAAACATCTCCTCAAGCCCTCAGATTGATTACCATGTCTTT 60
Db	1 ATGATGTGTTTCCTCGTTTAAACATCTCCTCAAGCCCTCAGATTGATTACCATGTCTTT 60
Oy	61 CTACTTCATTTCATGGTTCGTATCATCATGTCAAAGATTTTGACCTGACTCAAGTAGCATG 120
Db	61 CTACTTCATTTCATGGTTCGTATCATCATGTCAAAGATTTTGACCTGACTCAAGTAGCATG 120
Oy	121 ATCACTCCTTCATGCGCAAAAAGATATTTTCCCTGTGGGAATCTTAACAAGCTTACC 180
Db	121 ATCACTCCTTCATGCGCAAAAAGATATTTTCCCTGTGGGAATCTTAACAAGCTTACC 180
Oy	181 CGAGCTTTTCACTGTGATGCGAAGATGACTGTGGGAACGGGGCGGACGAAGAAGACTGT 240
Db	181 CGAGCTTTTCACTGTGATGCGAAGATGACTGTGGGAACGGGGCGGACGAAGAAGACTGT 240
Oy	241 GGTCACACTAGTGCATGGGCCAACATATTTGGCACATGTCATGGAATGCTAACACGCGTG 300
Db	241 GGTCACACTAGTGCATGGGCCAACATATTTGGCACATGTCATGGAATGCTAACACGCGTG 300
Oy	241 GGTCACACTAGTGCATGGGCCAACATATTTGGCACATGTCATGGAATGCTAACACGCGTG 300
Db	241 GGTCACACTAGTGCATGGGCCAACATATTTGGCACATGTCATGGAATGCTAACACGCGTG 300
Oy	301 GCCTTAACACAGAGAGTGCCTTTCTAAAAACAGTATCCAAGATGTCGACGCAAGAAACT 360
Db	301 GCCTTAACACAGAGAGTGCCTTTCTAAAAACAGTATCCAAGATGTCGACGCAAGAAACT 360
Oy	361 GAATTGGAATGTATAATGATGACTTTAAAGTCTGTGCCGATGATTTCTAACATGTGACA 420
Db	361 GAATTGGAATGTATAATGATGACTTTAAAGTCTGTGCCGATGATTTCTAACATGTGACA 420
Oy	421 TTACTGTCTCTTAAGAAAAACAAAATCCACAGTCTTCCAGATTAAGTTTTCTCAATATC 480
Db	421 TTACTGTCTCTTAAGAAAAACAAAATCCACAGTCTTCCAGATTAAGTTTTCTCAATATC 480
Oy	481 ACAAAACTTAAAAAAGATATTTCTTGACATATTTGACATATTCAGATATCCAGAAAGCA 540
Db	481 ACAAAACTTAAAAAAGATATTTCTTGACATATTTGACATATTCAGATATCCAGAAAGCA 540
Oy	541 TTTTGTGATTAATGTAAATCTGCAAAATATTAATATCTCAACACACACTGATCAACCCCTC 600
Db	541 TTTTGTGATTAATGTAAATCTGCAAAATATTAATATCTCAACACACACTGATCAACCCCTC 600
Oy	601 AGACCTGGAATATTAAGAAAGCTTAATCATGAGCTAACTTGGCTAAATCTAGATACATATCA 660
Db	601 AGACCTGGAATATTAAGAAAGCTTAATCATGAGCTAACTTGGCTAAATCTAGATACATATCA 660
Oy	661 ATAAACGAATTTCAACAGCGCTGTGTTACGGGATTTAAATTCCTGTGTTTCTGTCTATG 720
Db	661 ATAAACGAATTTCAACAGCGCTGTGTTACGGGATTTAAATTCCTGTGTTTCTGTCTATG 720

XX Feder JN, Mincier G, Ramanathan CS, Hawken DR;
XX MPI: 2002-435196/46.
XX P-PSDB: AAU97158.
XX Novel G protein-coupled receptor, HGRBMV5 polypeptide, useful for
XX treatment of AIDS, allergies, asthma, atherosclerosis, ulcerative
XX colitis, atopic dermatitis, diabetes mellitus, glomerulonephritis,
XX osteoarthritis -
XX
XX Claim 1; Fig 1; 148bp; English.
XX
XX The present invention relates to the isolation of a novel human
XX G-protein coupled receptor (GPCR) (HGRBMV5), and the polynucleotide
XX sequence encoding it. The HGRBMV5 polypeptide and polynucleotide
XX are useful for preventing, treating or ameliorating a disease,
XX disorder or condition related to the colon, brain, ovaries, thymus,
XX lungs or immune system. They are particularly useful for the
XX treatment or prevention of cancers, immune disorders, neurological
XX disorders, and diseases related to the brain, ovaries, thymus or
XX lungs. The polynucleotide sequence is useful for diagnosing or
XX determining susceptibility to infections such as bacterial, fungal,
XX protozoan and viral infections, particularly infections caused by
XX human immunodeficiency virus (HIV or HIV-2). The present sequence
XX encodes human GPCR HGRBMV5.
XX
SQ Sequence 2214 BP; 638 A; 457 C; 416 G; 703 T; 0 other;

Query Match 97.7%; Score 2214; DB 24; Length 2214;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 ATGCTCTTCTACTCATTTTCATGCTTGTGATGCAAGATTTTGCACTGACTCA 111
DB 1 ATGCTCTTCTACTCATTTTCATGCTTGTGATGCAAGATTTTGCACTGACTCA 60
QY 112 GGTAGCATGATCCTCTTCATGCCAAAAGATATTTTCCCTGTGGAACTTTACCAAG 171
DB 61 GGTAGCATGATCCTCTTCATGCCAAAAGATATTTTCCCTGTGGAACTTTACCAAG 120
QY 172 TGTCTTACCCCGAGCTTTTCACTGTATGAGCAAGATGACTGTGGAAAGGGCGGACGAA 231
DB 121 TGTCTTACCCCGAGCTTTTCACTGTATGAGCAAGATGACTGTGGAAAGGGCGGACGAA 180
QY 232 GAGAACTGTGACACTAGTGTGATGGGAGCAATATTTGGCAGTGTGAAATGCT 291
DB 181 GAGAACTGTGACACTAGTGTGATGGGAGCAATATTTGGCAGTGTGAAATGCT 240
QY 292 AACAGCGTGGCTTTAACAAGAGTCTTTCTAAAACAGTATCCAAATGCTGTGACTGC 351
DB 241 AACAGCGTGGCTTTAACAAGAGTCTTTCTAAAACAGTATCCAAATGCTGTGACTGC 300
QY 352 AAAAGAACTGAAATGTGTAAATGTGTAAAGTCTGTGTCCGATATTTTCTAAC 411
DB 301 AAAAGAACTGAAATGTGTAAATGTGTAAAGTCTGTGTCCGATATTTTCTAAC 360
QY 412 AATGTGACATTAAGTCTCTTAAGAAAAAACAATCCACAGTCTCCAGATTAAGTTTC 471
DB 361 AATGTGACATTAAGTCTCTTAAGAAAAAACAATCCACAGTCTCCAGATTAAGTTTC 420
QY 472 ATCAATATCACAAACCTTAAGAAATATTTCTTCAGCATTAATGTGATTAAGACATATCC 531
DB 421 ATCAATATCACAAACCTTAAGAAATATTTCTTCAGCATTAATGTGATTAAGACATATCC 480
QY 532 AGGAAGAGATTTTGTGATTAATGTAATCTGCAAAATTAATATCTCAACCAACTGCTATC 591
DB 481 AGGAAGAGATTTTGTGATTAATGTAATCTGCAAAATTAATATCTCAACCAACTGCTATC 540
QY 592 ACAACCTCAGACCTGAAATATTTCAAGACTTACATCAGCTAATCTGGCTAATTTAGAT 651
DB 541 ACAACCTCAGACCTGAAATATTTCAAGACTTACATCAGCTAATCTGGCTAATTTAGAT 600

QY 652 GACAATCCAAATTAACAGAAATTTACAGCGCTTTGTTAAGGATTAATTCCTGTGTTTC 711
DB 601 GACAATCCAAATTAACAGAAATTTACAGCGCTTTGTTAAGGATTAATTCCTGTGTTTC 660
QY 712 CTGTCTATGTTAATTAATTAATTAAGTCTTCCCAAGCAGATGTGTGCCAAATGCT 771
DB 661 CTGTCTATGTTAATTAATTAATTAAGTCTTCCCAAGCAGATGTGTGCCAAATGCT 720
QY 772 CAATCAACTGGGAGATTTGGAAGCAATGAAATTAAGTATCAATATTCACGTTT 831
DB 721 CAATCAACTGGGAGATTTGGAAGCAATGAAATTAAGTATCAATATTCACGTTT 780
QY 832 CTGTGTGCGAATGCTCACAGTCTGTCTGCTGAAATCAATATGTTTGTTC 891
DB 781 CTGTGTGCGAATGCTCACAGTCTGTCTGCTGAAATCAATATGTTTGTTC 840
QY 892 GAGAAACATTTTCTTCAATTAATAATTTAGAGAACTGATCTGTCTAGCAATACGTA 951
DB 841 GAGAAACATTTTCTTCAATTAATAATTTAGAGAACTGATCTGTCTAGCAATACGTA 900
QY 952 ACGAGCTATCACCTCACTTTTAAAGACTTGAAGCTTCAACAAAGCTGACCTGCA 1011
DB 901 ACGAGCTATCACCTCACTTTTAAAGACTTGAAGCTTCAACAAAGCTGACCTGCA 960
QY 1012 TCCAACTCTTATGATCTTCAACAGAACCAAGTTGAAAGCTTTAAACAATTCAGTCT 1071
DB 961 TCCAACTCTTATGATCTTCAACAGAACCAAGTTGAAAGCTTTAAACAATTCAGTCT 1020
QY 1072 CTAACTCTGGAAGAGATTAATTAATTAATTAACAGAAATGTTTCAACCACTGAAAG 1131
DB 1021 CTAACTCTGGAAGAGATTAATTAATTAATTAACAGAAATGTTTCAACCACTGAAAG 1080
QY 1132 AATCTTCTGCACTTTTCAAAAACCTTGTGATAGCTCTTATGCTCCCACTGCGCA 1191
DB 1081 AATCTTCTGCACTTTTCAAAAACCTTGTGATAGCTCTTATGCTCCCACTGCGCA 1140
QY 1192 ATATGATAGCCCTTGACGAGAGGCAATTTCTATTTGAGAGCTCTTGCTTAACAATATC 1251
DB 1141 ATATGATAGCCCTTGACGAGAGGCAATTTCTATTTGAGAGCTCTTGCTTAACAATATC 1200
QY 1252 CTGAGATTAATTTGTCTGAGGTTATAGCTTCAATTAACGCTTTTGTGATTT 1311
DB 1201 CTGAGATTAATTTGTCTGAGGTTATAGCTTCAATTAACGCTTTTGTGATTT 1260
QY 1312 GGCATGAGATCTTCAATTAAGCTGAAATCACTACAGCTATGTCATCAAAATCCTT 1371
DB 1261 GGCATGAGATCTTCAATTAAGCTGAAATCACTACAGCTATGTCATCAAAATCCTT 1320
QY 1372 TGTGTGTGATGCTCTGATGAGTGTGTTACTTGTCTTGTGCAATTTGATTAATAA 1431
DB 1321 TGTGTGTGATGCTCTGATGAGTGTGTTACTTGTCTTGTGCAATTTGATTAATAA 1380
QY 1432 TACGAGAGGCAATTAAGAGTATGCTGTGTGAGATGAGAACGTCAGTCCGCTC 1491
DB 1381 TACGAGAGGCAATTAAGAGTATGCTGTGTGAGATGAGAACGTCAGTCCGCTC 1440
QY 1492 ATGGGGTTCCTGGCCATGCTGTCCACAGAAAGTCTCTGTTCTGCTACTGACCTACTGACT 1551
DB 1441 ATGGGGTTCCTGGCCATGCTGTCCACAGAAAGTCTCTGTTCTGCTACTGACCTACTGACT 1500
QY 1552 TTGAGAAAGTTCCTGGTCATTTGCTTCCCTTCAATTAATTTGCACTGAGAAACGGCAG 1611
DB 1501 TTGAGAAAGTTCCTGGTCATTTGCTTCCCTTCAATTAATTTGCACTGAGAAACGGCAG 1560
QY 1612 ACCTCAGTATCCATTTGATGATGATGAGCGGAGTTTAAATAGCTGTAATTCATTT 1671
DB 1561 ACCTCAGTATCCATTTGATGATGATGAGCGGAGTTTAAATAGCTGTAATTCATTT 1620
QY 1672 TGAATTAAGATTTTGTGAAACCTTTAATGGAATAATGAGATGTTTCCACTTTAT 1731
DB 1621 TGAATTAAGATTTTGTGAAACCTTTAATGGAATAATGAGATGTTTCCACTTTAT 1680
QY 1732 TATGACCAACAGAAAGATTTGGAAGCAAGGATATTTCTTGGAAATTTTCTAGGTGTG 1791

Db 1681 TATGACCAACAGAGTATGGAGAAAGGATTCCTTGGAAATTTCCATAGGCTG 1740
Qy 1792 AACTTGTGCTTTTCTCATCATTTGTGTTTCTTATATATATATGTTCTGTCATTCAA 1851
Db 1741 AACTTGTGCTTTTCTCATCATTTGTGTTTCTTATATATATATGTTCTGTCATTCAA 1800
Qy 1852 AAAACGCGCTTGGAGACACAGAGTAAGAAATTTGTTTGGAGAGAGGCTGTGCA 1911
Db 1801 AAAACGCGCTTGGAGACACAGAGTAAGAAATTTGTTTGGAGAGAGGCTGTGCA 1860
Qy 1912 AATCGTTTCTTTTATATAGTGTCTCTGATGCCATCTGCTGATTCCTGTATTTGATGTT 1971
Db 1861 AATCGTTTCTTTTATATAGTGTCTCTGATGCCATCTGCTGATTCCTGTATTTGATGTT 1920
Qy 1972 AAAATCTTTCCTCTTCCGGGTGGAAATACACAGACCAATGACTTCTGATATGATGTT 2031
Db 1921 AAAATCTTTCCTCTTCCGGGTGGAAATACACAGACCAATGACTTCTGATATGATGTT 1980
Qy 2032 TTTTTCCTTCCAGTTACAGAGCTTTGAATCCATCTCTATATCTCTACACCAACTTT 2091
Db 1981 TTTTTCCTTCCAGTTACAGAGCTTTGAATCCATCTCTATATCTCTACACCAACTTT 2040
Qy 2092 TTTAAGACAAGTTGAAACAGCTGCTGACAAACATCAGAGAAATCAATTTCAAAAT 2151
Db 2041 TTTAAGACAAGTTGAAACAGCTGCTGACAAACATCAGAGAAATCAATTTCAAAAT 2100
Qy 2152 AAAAAAAGTTTAT 2211
Db 2101 AAAAAAAGTTTAT 2160
Qy 2212 GGGGTTTGAACAATAATACACTGAGAGACAGTATATGAACAGATTTCTAG 2265
Db 2161 GGGGTTTGAACAATAATACACTGAGAGACAGTATATGAACAGATTTCTAG 2214

RESULT 4
ABL40197 standard; cDNA; 2190 BP.
XX ABL40197;
AC ABL40197;
XX 23-MAY-2002 (first entry)
XX Human G protein-coupled receptor TGR17-6 encoding cDNA SEQ ID NO:16.
DE Human G protein-coupled receptor TGR17-6; noctropic; antiinflammatory;
KW vascotropic; immunomodulator; cytostatic; gene therapy; protein therapy;
KW neurological; inflammatory; circulatory; degenerative; immune system;
KW digestive disease; cancer; gene; ss.
XX Homo sapiens.
OS Homo sapiens.
XX Key CDS Location/Qualifiers
FT 1..2190
FT /*Lag= a
FT /partial
FT /product= "TGR17-6"
FT /note= "no stop codon given"
XX
XX NO200204640-A1.
XX 17-JAN-2002.
XX 06-JUL-2001; 2001WO-JP05878.
XX 07-JUL-2000; 2000JP-0211989.
XX 18-DEC-2000; 2000JP-0383794.
XX (TAKE) TAKEDA CHEM IND LTD.
XX PA
XX PI Moriya T, Ito T, Shintani Y, Miyajima N;

DR WPI: 2002-179706/23.
DR P-PsDB; ABB06255.
XX G-protein coupled receptor protein TGR17 of human origin and DNA
PT encoding it for diagnosis and treatment of cancer and circulatory and
PT other diseases associated with its expression -
XX
XX Claim 7; Page 135-136; 145pp; Japanese.
XX The present invention describes a human guanine nucleotide binding
CC protein (G protein) coupled receptor protein designated TGR17, which has
CC 5 variant forms (TGR17-1 to TGR17-5) of the receptor protein having
CC additional residues at the N-terminal. The TGR17 proteins have noctropic,
CC antiinflammatory, vasotropic, immunomodulator and cytostatic activities.
CC The TGR17 polynucleotides and protein can be used in gene therapy and
CC protein therapy. G-protein coupled receptor proteins are cell membrane
CC proteins mediating the cellular response to a large variety of signaling
CC molecules. The TGR17 polynucleotides and proteins can be used in the
CC diagnosis, treatment and prevention of diseases including neurological,
CC inflammatory, circulatory, degenerative, immune system and digestive
CC diseases and cancer. The present sequence encodes human TGR17-6 from the
CC present invention.
XX
XX Sequence 2190 BP; 626 A; 457 C; 409 G; 698 T; 0 other;
SQ
Query Match 92.9%; Score 2104.8; DB 24; Length 2190;
Best Local Similarity 96.7%; Pred. No. 0;
Matches 2188; Conservative 0; Mismatches 2; Indels 72; Gaps 1;
Qy 1 ATGATGTTTTTCTGTTTTTAAACATCTCTTCAAGCTCAGATTGATTAATATTTCTTT 60
Db 1 ATGATGTTTTTCTGTTTTTAAACATCTCTTCAAGCTCAGATTGATTAATATTTCTTT 60
Qy 61 CTACTCATTTTCACTGTTTCAATGTCATTAAGTTCATTAAGTTCATTAAGTTCATTAAG 120
Db 61 CTACTCATTTTCACTGTTTCAATGTCATTAAGTTCATTAAGTTCATTAAGTTCATTAAG 120
Qy 121 ATCACTCTTTCATGCGCAAAAGATTTTCCCTGCGGAAATCTTCAAGTCTTAACCC 180
Db 121 ATCACTCTTTCATGCGCAAAAGATTTTCCCTGCGGAAATCTTCAAGTCTTAACCC 180
Qy 181 CGAGCTTTTCACTGTTTCAATGTCATTAAGTTCATTAAGTTCATTAAGTTCATTAAG 240
Db 181 CGAGCTTTTCACTGTTTCAATGTCATTAAGTTCATTAAGTTCATTAAGTTCATTAAG 240
Qy 241 GGTGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
Db 241 GGTGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
Qy 301 GCCTTAACACAGAGAGTCTTTCTTAAACAGTATCCCAATGCTGTGACTGCAAGAACT 360
Db 301 GCCTTAACACAGAGAGTCTTTCTTAAACAGTATCCCAATGCTGTGACTGCAAGAACT 360
Qy 361 GAATGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
Db 361 GAATGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
Qy 421 TTACTGTCTTAAAGAAAAAACAATTCACAGTCTTCAAGTATTAAGTTCATTAAGTTC 480
Db 421 TTACTGTCTTAAAGAAAAAACAATTCACAGTCTTCAAGTATTAAGTTCATTAAGTTC 480
Qy 481 ACAAACCTTAAAGATATTTCTTCAAGTATTAAGTTCATTAAGTTCATTAAGTTCATTAAG 540
Db 481 ACAAACCTTAAAGATATTTCTTCAAGTATTAAGTTCATTAAGTTCATTAAGTTCATTAAG 540
Qy 541 TTTTGTGATATGATATGCAAAATATATATCTCAACCAACATGCAATCAACCTTC 600
Db 541 TTTTGTGATATGATATGCAAAATATATATCTCAACCAACATGCAATCAACCTTC 600
Qy 601 AGACTGGAATATTTCAAGATTAATCACTGATCTTGGCTAATTTCTAATGATGATCA 660
Db 601 AGACTGGAATATTTCAAGATTAATCACTGATCTTGGCTAATTTCTAATGATGATCA 660

Qy	661	ATAACGAATTTTCAACAGCGCTGTGTTTACGGGATTAATATCTGTTTTCCTGTATG	720
Dp	661	ATAACCGAATTTTCAACAGCGCTGTGTTTACGGGATTAATATCTGTTTTCCTGTATG	720
Qy	721	GTTAATACTACTAGAAAGCTCTTCCAGAGCAGATGTGTGCCAAATGCTCACTCAAC	780
Dp	721	GTTAATACTACTAGAAAGCTCTTCCAGAGCAGATGTGTGCCAAATGCTCACTCAAC	780
Qy	781	TGGGTGATTTTGGAAAGCAATAGAAATTAAGTATCTCAAAATTTCTAGCTTTCTGTGC	840
Dp	781	TGGGTGATTTTGGAAAGCAATAGAAATTAAGTATCTCAAAATTTCTAGCTTTCTGTGC	840
Qy	841	GATTGCGCTCAACAGTCTGTCTTCTCGCTAGAAATCAAAATGGTTTGTTCAGAGAAACA	900
Dp	841	GATTGCGCTCAACAGTCTGTCTTCTCGCTAGAAATCAAAATGGTTTGTTCAGAGAAACA	900
Qy	901	TTTTCTTCATTTAAAAAATTTAGAGAACTGGATCTGTCTAGCAATACGATACGAGCTA	960
Dp	856	-----CTGGATCTGTCTAGCAATACGATACGAGCTA	888
Qy	961	TCACCTCACTCTTTTAAAAAGCTTGAAGCTTCAAAAAGCTGAACCTGTCACTCACTCT	1020
Dp	889	TCACCTCACTCTTTTAAAAAGCTTGAAGCTTCAAAAAGCTGAACCTGTCACTCACTCT	948
Qy	1021	CTTATGTATCTTCAACAAGACCAAGTTGAAAGCTTAAACAATTCAGTCTTAGACCTG	1080
Dp	949	CTTATGTATCTTCAACAAGACCAAGTTGAAAGCTTAAACAATTCAGTCTTAGACCTG	1008
Qy	1081	GAAAGGATAGAGATTTCCAAATATTAACAACAGAAATGTTCAACCCATGAAGAACTCTCT	1140
Dp	1009	GAAAGGATAGAGATTTCCAAATATTAACAACAGAAATGTTCAACCCATGAAGAACTCTCT	1068
Qy	1141	CACATTTATTTCAAAAACTTTCGATCTAGTCTCTATGCTCCCAATGTCCGAATATGTATG	1200
Dp	1069	CACATTTATTTCAAAAACTTTCGATCTAGTCTCTATGCTCCCAATGTCCGAATATGTATG	1128
Qy	1201	CCCTTGAGAGCAGGATTTCTTCATTTGAGAGCCTCTTGSGTAAACATATCTCAGATA	1260
Dp	1129	CCCTTGAGAGCAGGATTTCTTCATTTGAGAGCCTCTTGSGTAAACATATCTCAGATA	1188
Qy	1261	TTTGTCTGGGTTATAGCTTTCATTAACCTGCTTGGAATCTTTTGTGTCATTTGGCATAGA	1320
Dp	1189	TTTGTCTGGGTTATAGCTTTCATTAACCTGCTTGGAATCTTTTGTGTCATTTGGCATAGA	1248
Qy	1321	TCTTTCAATTAAGCTGAATAATCAACTACGCTATGTCCATCAAAATCTTTGTGTGCT	1380
Dp	1249	TCTTTCAATTAAGCTGAATAATCAACTACGCTATGTCCATCAAAATCTTTGTGTGCT	1308
Qy	1381	GATTGCCGATAGGGGTTTACTGTCTCTTGTTGGCATTTTGGATATTAATAACCGAGGG	1440
Dp	1309	GATTGCCGATAGGGGTTTACTGTCTCTTGTTGGCATTTTGGATATTAATAACCGAGGG	1368
Qy	1441	CAGTATCAGAAAGTATGCTTGTGATGAGAGAGCGTGCAGTGCCTCATGGGGTTC	1500
Dp	1369	CAGTATCAGAAAGTATGCTTGTGATGAGAGAGCGTGCAGTGCCTCATGGGGTTC	1428
Qy	1501	CTGGCAGAGCTGTCCACGGAAGCTCTCTCTTCTGCTACAGACCTTCACTTGGAAAG	1560
Dp	1429	CTGGCAGAGCTGTCCACGGAAGCTCTCTCTTCTGCTACAGACCTTCACTTGGAAAG	1488
Qy	1561	TTTCCGTGATATGTCTTCCCTTCAGTAAACTTCGACTCTGAAAAACGGCAGACCTCAGTC	1620
Dp	1489	TTTCCGTGATATGTCTTCCCTTCAGTAAACTTCGACTCTGAAAAACGGCAGACCTCAGTC	1548
Qy	1621	ATCTCATTTTGCATCTGATGAGCGGGATTTTAAATAGCTGTAAATTCATTTGGAAATAG	1680
Dp	1549	ATCTCATTTTGCATCTGATGAGCGGGATTTTAAATAGCTGTAAATTCATTTGGAAATAG	1608
Qy	1681	GATTAATTTTGGAAACTTTTATGAGAAAAATGGAAGTATGTTTCCACTTATTAATGACCAA	1740
Dp	1609	GATTAATTTTGGAAACTTTTATGAGAAAAATGGAAGTATGTTTCCACTTATTAATGACCAA	1668
Qy	1741	ACAGAAGATTTGGAACAAAGGGATTTCTCTTGGAATTTTCTCTAGTGTGAACCTTGCTG	1800

Dd		1669	ACAGAAATGATTGGAACCAAGGATATCTCTTGGAATTTTCCTAGGTGTGAACTTCCTG	1728
Oy		1801	GCTTTTCTCATCATGTGTTTTTCCATAATTAATAATGTTCTGTTCCATTCAA AAAAACC GCC	1860
Dd		1729	GCTTTTCTCATCATGTGTTTTTCCATAATTAATAATGTTCTGTTCCATTCAA AAAAACC GCC	1788
Oy		1861	TTTGAGAGCCACAGAAATGAAGAATGTTTTGGAAGAGAGGCGTGTGCAAAATCGTTTC	1920
Dd		1789	TTTGAGAGCCACAGAAATGAAGAATGTTTTGGAAGAGAGGCGTGTGCAAAATCGTTTC	1848
Oy		1921	TTTTTTTAAAGTGTCTCTGATGCCATCTGCTGGAATTCCTGTATTTGTAGTTAAAATCCTT	1980
Dd		1849	TTTTTTTAAAGTGTCTCTGATGCCATCTGCTGGAATTCCTGTATTTGTAGTTAAAATCCTT	1908
Oy		1981	TCCCTCTTCGGGGTGGAAAAATPACAAGACAATAATGACTTCCTGGAAAGATATTTTTCCTT	2040
Dd		1909	TCCCTCTTCGGGGTGGAAAAATPACAAGACAATAATGACTTCCTGGAAAGATATTTTTCCTT	1968
Oy		2041	CCAATTAAACAGTGCCTTTGAAATCCAAATCCTGTATCTCTCAACCAACTTTTAAAGAC	2100
Dd		1969	CCAATTAAACAGTGCCTTTGAAATCCAAATCCTGTATCTCTCAACCAACTTTTAAAGAC	2028
Oy		2101	AAGTTGAAACAGCTGCTGCGACAAACATCACAGAAATCAATTTCAA AATTA AAAAAA	2160
Dd		2029	AAGTTGAAACAGCTGCTGCGACAAACATCACAGAAATCAATTTCAA AATTA AAAAAA	2088
Oy		2161	AGTTTATCTACATCATCTGTGTGTGATGAGAGACTCCCTCTCCCTGAAACTTG GGG GTT TG	2220
Dd		2089	AGTTTATCTACATCATCTGTGTGTGATGAGAGACTCCCTCTCCCTGAAACTTG GGG GTT TG	2148
Oy		2221	AACAAATTAACACTTGGAGACAGTAAATGAAGAAACCAATTTCC	2262
Dd		2149	AACAAATTAACACTTGGAGACAGTAAATGAAGAAACCAATTTCC	2190
RESULT 5				
ABKS1947		ID	ABKS1947; standard; cDNA; 2142 BP.	
XX		AC	ABKS1947;	
XX		DT	27-AUG-2002 (first entry)	
DE		CDNA	encoding human G-protein coupled receptor HGRBMY5 splice variant.	
XX		Human; G-protein coupled receptor; GPCR; HGRBMY5; colon; brain;		
KW		ovary; thymus; lung; immune system; cancer; immune disorder;		
KM		neurological disorder; infection; human immunodeficiency virus; HIV;		
KM		antiallergic; antiaesthetic; dermatological; antiarteriosclerotic;		
KM		antidiabetic; nephrotropic; osteopathic; antiarthritic;		
KM		antiinflammatory; antirheumatic; antichydroid; cytosolic; valnery;		
KW		vitruclide; antibacterial; antifungal; antiparasitic; protozoicide;		
KM		antihelminthic; nootropic; neuroprotective; antidepressant;		
XX		anticomvulsant; antiparkinsonian; neuroleptic; anti-HIV; gene; ss.		
OS		Homo sapiens.		
FH		Key	Location/Qualifiers	
FT		CDS	1..2142	
FT		/tag= a		
FT		/product= "GPCR HGRBMY5"		
PN		WO200226824-A2.		
XX		PD	04-APR-2002.	
XX		PF	26-SEP-2001; 2001WO-US30365.	
PR		27-SEP-2000; 2000US-235713P.		
PR		16-JAN-2001; 2001US-261781P.		
PR		19-JUL-2001; 2001US-306605P.		
PR		03-AUG-2001; 2001US-310436P.		

XX (BRIM) BRISTOL-MYERS SQUIBB CO.
XX Feder JN, Mintier G, Ramanathan CS, Hawken DR;
XX WPI; 2002-435196/46.
XX P-PSDB; AAU97159.
XX
XX Novel G protein-coupled receptor, HGPBMY5 polypeptide, useful for
XX treatment of AIDS, allergies, asthma, atherosclerosis, ulcerative
XX PT colitis, atopic dermatitis, diabetes mellitus, glomerulonephritis,
XX PT osteoarthritis -
XX
XX Claim 1; Fig 5; 148pp; English.
XX
XX The present invention relates to the isolation of a novel human
XX G-protein coupled receptor (GPCR) (HGPBMY5), and the polynucleotide
XX sequence encoding it. The HGPBMY5 polypeptide and polynucleotide
XX are useful for preventing, treating or ameliorating a disease,
XX disorder or condition related to the colon, brain, ovaries, thymus,
XX lungs or immune system. They are particularly useful for the
XX treatment or prevention of cancers, immune disorders, neurological
XX disorders, and diseases related to the brain, ovaries, thymus or
XX lungs. The polynucleotide sequence is useful for diagnosing or
XX determining susceptibility to infections such as bacterial, fungal,
XX CC protozoan and viral infections, particularly infections caused by
XX human immunodeficiency virus (HIV or HIV-2). The present sequence
XX encodes a splice variant of human GPCR HGPBMY5.
XX
XX Sequence 2142 BP; 613 A; 435 C; 408 G; 686 T; 0 other;
SQ
Query Match 90.9%; Score 2060; DB 24; Length 2142;
Best Local Similarity 96.7%; Pred. No. 0;
Matches 2142; Conservative 0; Mismatches 0; Indels 72; Gaps 1;
QY 52 ATGTTCTTCTACTTCAATTCATGCTCTGATCAATGTCAAAGATTTTGGACTGACTCAA 111
DB 1 ATGTTCTTCTACTTCAATTCATGCTCTGATCAATGTCAAAGATTTTGGACTGACTCAA 60
QY 112 GGTAGCATGATCACTCTTCAATGCGCAAAAGATATTTTCCCTGTGGAAATCTTACCAAG 171
DB 61 GGTAGCATGATCACTCTTCAATGCGCAAAAGATATTTTCCCTGTGGAAATCTTACCAAG 120
QY 172 TGCTTACCCGAGCTTTTCACTGTGATGGCAAGGATGACTGTGGGAACTGGGAGGAGGAA 231
DB 121 TGCTTACCCGAGCTTTTCACTGTGATGGCAAGGATGACTGTGGGAACTGGGAGGAGGAA 180
QY 232 GAGAATCTGTGGTGAACACTAGTGAATGGGCGACATATTTTGGCAAGTGAATAGCT 291
DB 181 GAGAATCTGTGGTGAACACTAGTGAATGGGCGACATATTTTGGCAAGTGAATAGCT 240
QY 292 AACAGCGTGGCTTAAACACAGAGATGCTTTTAAACAGATTCACAAATGTGTGATGCT 351
DB 241 AACAGCGTGGCTTAAACACAGAGATGCTTTTAAACAGATTCACAAATGTGTGATGCT 300
QY 352 AAAGAACTGAATGGAATGTGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAAT 411
DB 301 AAAGAACTGAATGGAATGTGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAAT 360
QY 412 AATGTGACATTAATGCTCTTAAAGAAACAAATTCACAGTCTTCCAGATTAAGTTTTC 471
DB 361 AATGTGACATTAATGCTCTTAAAGAAACAAATTCACAGTCTTCCAGATTAAGTTTTC 420
QY 472 ATCAAAATACCAAAATCTTAAAGATATTTCTTGAATTAATGCAATTAATGCAATTAATG 531
DB 421 ATCAAAATACCAAAATCTTAAAGATATTTCTTGAATTAATGCAATTAATGCAATTAATG 480
QY 532 AGGAATCAATTTTGGATTAATGTAATCTGCAATATATTAATCTCAACCAATGTCATC 591
DB 481 AGGAATCAATTTTGGATTAATGTAATCTGCAATATAT----- 517
QY 592 ACAACCTCAGACCTGGAATATTCAGAAAGATTACATCAGCTTAATGCTTAATCTAGAT 651
|||||

DB 518 -----TAATCTAGAT 528
QY 652 GACAAATCCAAATACCAAGATTTTCAAGCGCTTGTATTACGGGATTAATTCCTTTGTTTC 711
DB 529 GACAAATCCAAATACCAAGATTTTCAAGCGCTTGTATTACGGGATTAATTCCTTTGTTTC 588
QY 712 CTGTCTATGTTTAATTAATCTAGTGAAGCTTCTCCCAAGCAATGATGATCCCAATAGCTT 771
DB 589 CTGTCTATGTTTAATTAATCTAGTGAAGCTTCTCCCAAGCAATGATGATCCCAATAGCTT 648
QY 772 CAATCAATCTGGGTGATTTGGAAGCAATAGAAATTAATATCTCAAAATCTCAAGTTT 831
DB 649 CAATCAATCTGGGTGATTTGGAAGCAATAGAAATTAATATCTCAAAATCTCAAGTTT 708
QY 832 CTGTCTATGTTTAATTAATCTAGTGAAGCTTCTCCCAAGCAATGATGATCCCAATAGCTT 891
DB 709 CTGTCTATGTTTAATTAATCTAGTGAAGCTTCTCCCAAGCAATGATGATCCCAATAGCTT 768
QY 892 GAGAAACATTTTCTTCAATTAATAATTTAGAGAACTGATCTGTCTAGCAATAGATTA 951
DB 769 GAGAAACATTTTCTTCAATTAATAATTTAGAGAACTGATCTGTCTAGCAATAGATTA 828
QY 952 ACGAGACTATCACTTCACTTTTAAAGCTTGAAGCTTCTCAAAAGCTGAACTGTCA 1011
DB 829 ACGAGACTATCACTTCACTTTTAAAGCTTGAAGCTTCTCAAAAGCTGAACTGTCA 888
QY 1012 TCCATATCTTATGTAATCTTCAAGAAACCAAGTTGAAAGCTTAAACAATCTGATCT 1071
DB 889 TCCATATCTTATGTAATCTTCAAGAAACCAAGTTGAAAGCTTAAACAATCTGATCT 948
QY 1072 CTAGACCTGAAAGATAGATATTCGAATATTAACAACAGATGTTTCAACCCATGAAG 1131
DB 949 CTAGACCTGAAAGATAGATATTCGAATATTAACAACAGATGTTTCAACCCATGAAG 1008
QY 1132 AATCTTCTCACTTATTTTCAAAAATTTTGAATCTGTCTATGCTCCCATGTCCGA 1191
DB 1009 AATCTTCTCACTTATTTTCAAAAATTTTGAATCTGTCTATGCTCCCATGTCCGA 1068
QY 1192 ATATGTAATCCCTTGAACGAGCAATTTCTCAATTTGAAGACCTCTTGGCTAACATATTC 1251
DB 1069 ATATGTAATCCCTTGAACGAGCAATTTCTCAATTTGAAGACCTCTTGGCTAACATATTC 1128
QY 1252 CTCGAATATTTTGTCTGGGTATATGCTTCAATTAATCTGCTTGAATCTTTTGTGATCT 1311
DB 1129 CTCGAATATTTTGTCTGGGTATATGCTTCAATTAATCTGCTTGAATCTTTTGTGATCT 1188
QY 1312 GGCATGAGATCTTCAATTAAGCTGAAATTAACAATCAAGCTATGTCATCAAAATCTCT 1371
DB 1189 GGCATGAGATCTTCAATTAAGCTGAAATTAACAATCAAGCTATGTCATCAAAATCTCT 1248
QY 1372 TGTGTGCTGATGCTGATGAGTGTGTTTCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1431
DB 1249 TGTGTGCTGATGCTGATGAGTGTGTTTCTTGTGTTGTTGTTGTTGTTGTTGTTGTT 1308
QY 1432 TACCGAGGAGATGATGAGATGATGCTTGTGCTGATGATGAGAGAGCTGAGAGCTGCT 1491
DB 1309 TACCGAGGAGATGATGAGATGATGCTTGTGCTGATGATGAGAGAGCTGAGAGCTGCT 1368
QY 1492 ATGGGCTTCTGAGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1551
DB 1369 ATGGGCTTCTGAGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1428
QY 1552 TTGGAAGATTTCTGCTGATGCTTCCCTTCAAGTAACTTGAATGCTGCTGCTGCTGCT 1611
DB 1429 TTGGAAGATTTCTGCTGATGCTTCCCTTCAAGTAACTTGAATGCTGCTGCTGCTGCT 1488
QY 1612 ACCTGAGTCAATCTTCAATTTGATGATGATGATGATGATGATGATGATGATGATGAT 1671
DB 1489 ACCTGAGTCAATCTTCAATTTGATGATGATGATGATGATGATGATGATGATGATGAT 1548
QY 1672 TGAATTAAGATTTTGGAAATTTTGAATTTTGAATTTTGAATTTTGAATTTTGAATTTTGA 1731
DB 1549 TGAATTAAGATTTTGGAAATTTTGAATTTTGAATTTTGAATTTTGAATTTTGAATTTTGA 1608
|||||

QY 1732 TATGACCAACAGAGATATTGGAAGCAAGGTAATCTCTTGAATTTCTAGGTG 1791
Db 1609 TATGACCAACAGAGATATTGGAAGCAAGGTAATCTCTTGAATTTCTAGGTG 1668
QY 1792 AACTGTGCTCTTCTCATCTGTTTCTATATATTAATGTTCTGTTCAATCAA 1851
Db 1669 AACTGTGCTCTTCTCATCTGTTTCTATATATTAATGTTCTGTTCAATCAA 1728
QY 1852 AAAACCGCTTGCAGACCAAGAAATGTTTGAAGAGAGTGGCTGTTGCA 1911
Db 1729 AAAACCGCTTGCAGACCAAGAAATGTTTGAAGAGAGTGGCTGTTGCA 1788
QY 1912 AATGTTCTTTTATATAGTCTCTGATGCAATCTGTAATCTGTAATGTTAGTT 1971
Db 1789 AATGTTCTTTTATATAGTCTCTGATGCAATCTGTAATCTGTAATGTTAGTT 1848
QY 1972 AAAATCTCTTCTCTTCCGGGTGAAATACCAAGCAATGACTTCTGATAGTANT 2031
Db 1849 AAAATCTCTTCTCTTCCGGGTGAAATACCAAGCAATGACTTCTGATAGTANT 1908
QY 2032 TTTTCTCTGCAAGTAAAGTCTTGAATCCATCTCTTACTCTGACCAACCACTTT 2091
Db 1909 TTTTCTCTGCAAGTAAAGTCTTGAATCCATCTCTTACTCTGACCAACCACTTT 1968
QY 2092 TTTAAGCAAGTAAAGTCTGCTGCAAAACATCAGAGAAATCAATTTCAAATTT 2151
Db 1969 TTTAAGCAAGTAAAGTCTGCTGCAAAACATCAGAGAAATCAATTTCAAATTT 2028
QY 2152 AAAAAAAGTTTATCTACATCATCTGTTGATAGAGACTCTCTTCCCTGAAACTT 2211
Db 2029 AAAAAAAGTTTATCTACATCATCTGTTGATAGAGACTCTCTTCCCTGAAACTT 2088
QY 2212 GGGTTTGAACAAATAAAGTCTGGAAGCAATGAAACCAATTTCTCTAG 2265
Db 2089 GGGTTTGAACAAATAAAGTCTGGAAGCAATGAAACCAATTTCTCTAG 2142
RESULT 6
AAFB8580
ID AAFB8580 standard; cDNA; 2181 BP.
XX AAFB8580;
AC
XX
DT 19-NOV-2002 (first entry)
XX
DE Human GCRC-1 cDNA INCYTE ID 7485090CD1 SEQ ID 49.
XX
XX GCRC; Human; G-protein coupled receptor; anti-HIV; antiarteriosclerotic;
XX cytosolic; neuroprotective; antiparkinsonian; hepatocytotoxic; laxative;
XX cerebroprotective; antiinflammatory; virucide; antibacterial; fungicide;
XX procoagulant; cirrhosis; cancer; stroke; Alzheimer's disease; AIDS;
XX Parkinson's disease; Crohn's disease; constipation; infection;
XX gene therapy; gene; ss.
XX
OS Homo sapiens.
XX
XX WO200263004-A2.
XX
XX 15-AUG-2002.
XX
XX
XX 06-FEB-2002; 2002WO-US03635.
XX
XX 07-FEB-2001; 2001US-267322P.
XX 23-FEB-2001; 2001US-271215P.
XX 08-MAR-2001; 2001US-274551P.
XX 23-MAR-2001; 2001US-278507P.
XX 30-MAR-2001; 2001US-280597P.
XX 02-APR-2001; 2001US-281107P.
XX 06-APR-2001; 2001US-282121P.
XX
XX (INCY-) INCYTE GENOMICS INC.
XX

PI Baughn MR, Tribouley CM, Nguyen DB, Thornton M, Yao MG;
PI Kallik DA, Gandhi AR, Walla NK, Arvizu C, Elliott VS;
PI Harelia A, Ramkumar J, Pei J, Tang YT, Yue H, Reddy R;
PI Butford N, Lu DM, Gaul RC, Khan FA, Walsh RT, Ison CH;
PI Richardson TW, Griffin JA, Warren BA, Yang J, Lee EA, Harland L;
XX
XX MPI; 2002-62757/67.
XX
XX P-PSDB; AAB71322.
XX
XX New human G-protein coupled receptors (GCRC), useful for diagnosing or
XX treating a disease or condition associated with decreased expression or
XX over expression of functional GCRCs e.g. cancer, Alzheimer's and
XX Parkinson's -
XX
XX Claim 110; Page 209-210; 239pp; English.

XX
XX This invention describes novel polypeptides which have anti-HIV,
XX antiarteriosclerotic, cytosolic, neuroprotective, antiparkinsonian,
XX hepatocytotoxic, laxative, cerebroprotective, antiinflammatory, virucide,
XX antibacterial, fungicide and procoagulant activity. The products of the
XX invention are useful for treating a disease or condition associated with
XX decreased expression or over expression of functional G-protein coupled
XX receptors (GCRC), while antibodies generated against the polypeptide of
XX the invention are useful for diagnosing a condition or disease associated
XX with the expression of GCRC e.g. arteriosclerosis, cirrhosis, cancer,
XX stroke, Alzheimer's disease, Parkinson's disease, Crohn's disease,
XX constipation, AIDS, or bacterial, viral, fungal or protozoal infections.
XX The compound described in the invention can be used for gene therapy.
XX AAFB8580-AAB71322 encode the GCRC proteins represented by
XX AAB71322-AAB71369, described in the disclosure of the invention.
XX
XX Sequence 2181 BP; 635 A; 451 C; 419 G; 676 T; 0 other;

Query Match 88.4%; Score 2002.2; DB 24; Length 2181;
Best Local Similarity 95.4%; Pred. No. 0;
Matches 2114; Conservative 0; Mismatches 23; Indels 78; Gaps 2;

QY 57 CTTTCTACTTCAATTCATCGTTCTGATCAATGCAAGATTTTGCAGTCAAGGTAG 116
Db 39 CATGATTTAGTGTCAAAATGATGACAGTATGATTTTGCAGTCAAGGTAG 98
QY 117 CATGATCACTCTTCATGCAAAAGATTTTCTGTTGGAATCTTACCAAGTCTT 176
Db 99 CATGATCACTCTTCATGCAAAAGATTTTCTGTTGGAATCTTACCAAGTCTT 158
QY 177 ACCCGAGCTTTTACGTTGATGCAAGATGACGTTGGGAACGGGGGCGAGAGAA 236
Db 159 ACCCGAGCTTTTACGTTGATGCAAGATGACGTTGGGAACGGGGGCGAGAGAA 218
QY 237 CTGTGTGACACTAGTGTGATGGGACCAATTTTGGCAAGTGAAGAAATGCTAACG 296
Db 219 CTGTGTGACACTAGTGTGATGGGACCAATTTTGGCAAGTGAAGAAATGCTAACG 278
QY 297 CGTGGCTTTAACAAGAGTCTTTCTAACAAGTATCAAAATGCTGTGACTGAAGA 356
Db 279 CGTGGCTTTAACAAGAGTCTTTCTAACAAGTATCAAAATGCTGTGACTGAAGA 338
QY 357 AACTGAATTTGAATGTTGAATGGAAGTAAAGTCTGTCGAGATTTCTAACATGT 416
Db 339 AACTGAATTTGAATGTTGAATGGAAGTAAAGTCTGTCGAGATTTCTAACATGT 398
QY 417 GACATTTACTGTCTTTAAGAAACAAATTCACAGTCTTCAGATTAAGTTTCATCA 476
Db 399 GACATTTACTGTCTTTAAGAAACAAATTCACAGTCTTCAGATTAAGTTTCATCA 458
QY 477 ATACCAAAACTTAAAGATTTTCTTACATTAATGCAATTTAGCAATATTCAGAA 536
Db 459 ATACCAAAACTTAAAGATTTTCTTACATTAATGCAATTTAGCAATATTCAGAA 518
QY 537 AGCATTTTGTGATTAATGCAAAATTTAATCTCAACCAACATGATCAAC 596
Db 519 AGCATTTTGTGATTAATGCAAAATTTAATCTCAACCAACATGATCAAC 578

QY 597 CCTCAGACCTGGAAATTTTCAAGAATTACATGACGCTAATCTGATGACAA 656
 DB 579 CCTCAGACCTGGAAATTTTCAAGAATTACATGACGCTAATCTGATGACAA 638
 QY 657 TCCCAATTAACAGAAATTTTCAAGCGCTGTTTACGCGGATTAATTCCTGTTTTCTGTC 716
 DB 639 TCCCAATTAACAGAAATTTTCAAGCGCTGTTTACGCGGATTAATTCCTGTTTTCTGTC 698
 QY 717 TATGCTTAATTAACGCTTTTCCCAAGCAGATGTCGCCAATGCTCAACT 776
 DB 699 TATGCTTAATTAACGCTTTTCCCAAGCAGATGTCGCCAATGCTCAACT 758
 QY 777 CAACCTGGGATTTTGGAAAGGCAATGAATTAAGTCTCACAAAATTCAGCTTCTGTC 836
 DB 759 CAACCTGGGATTTTGGAAAGGCAATGAATTAAGTCTCACAAAATTCAGCTTCTGTC 818
 QY 837 GTGCGATTCGCTCACAGTCTGTTTCTGCTGAAATCAAAATGTTTTGTTCCAGAGAA 896
 DB 819 GTGCGATTCGCTCACAGTCTGTTTCTGCTGAAATCAAAATGTTTTGTTCCAGAGAA 837
 QY 897 GACATTTCTTCAATTAATAAATTTAGAGAACTGATCTGCTAGCAATGATTAACGGA 956
 DB 838 -----CTGATCTGCTAGCAATGATTAACGGA 866
 QY 957 GCTATCACTCACTTTTAAAGCTTGAAGCTTCAAAAAGCTGAACCTGCTCACTCA 1016
 DB 867 ACTATACCTCACTTTTAAAGCTTGAAGCTTCAAAAAGCTGAACCTGCTCACTCA 926
 QY 1017 TCCCTTAATGATCTTCAAGAAACAGTTTGAAGCTTAAACAATTCAGTCTCTAGA 1076
 DB 927 TCCCTTAATGATCTTCAAGAAACAGTTTGAAGCTTAAACAATTCAGTCTCTAGA 986
 QY 1077 CCTGGAAGAGATGAGATTCGAAATTAACAACAGATGTTCAACCCATGAAGATCT 1136
 DB 987 CCTGGAAGAGATGAGATTCGAAATTAACAACAGATGTTCAACCCATGAAGATCT 1046
 QY 1137 TTCTCAGAT-----TTAATTCAAAAAAGTTGATCTGCTGATGCTCCCATGTCG 1190
 DB 1047 TTCTCAGATCTGATTTATTTCAAAAAGTTGATCTGCTGATGCTCCCATGTCG 1106
 QY 1191 AATATGATGCTCTTGAACGAGCGGCAATTTCTGATTTAGAGACCTTGTGCTAACAATAT 1250
 DB 1107 AATATGATGCTCTTGAACGAGCGGCAATTTCTGATTTAGAGACCTTGTGCTAACAATAT 1166
 QY 1251 CCTCAGAAATTTGCTGCGGTTATAGCTTCACTGCTGTTGGAATTTTGTGCTAT 1310
 DB 1167 CCTCAGAAATTTGCTGCGGTTATAGCTTCACTGCTGTTGGAATTTTGTGCTAT 1226
 QY 1311 TGGCATGAGATCTTTCATTAAGCTGAATAATACAGCTATGTCATCAAAATCCT 1370
 DB 1227 TGGCATGAGATCTTTCATTAAGCTGAATAATACAGCTATGTCATCAAAATCCT 1286
 QY 1371 TTGTTGCTGATGCTGCTGATGAGGTTTAACTTGTCTTTGTTGCAATTTTGAATAAA 1430
 DB 1287 TTGTTGCTGATGCTGCTGATGAGGTTTAACTTGTCTTTGTTGCAATTTTGAATAAA 1346
 QY 1431 ATACCGAGGCAATATACAGAAATATGCTGCTGATGAGAGAGAGCTGAGAGCGCCCT 1490
 DB 1347 ATACCGAGGCAATATACAGAAATATGCTGCTGATGAGAGAGAGCTGAGAGCGCCCT 1406
 QY 1491 CATGGGTTCTGCGCAGCTGCTGTCACCGAAGTCTGTTCTGCTACTGACTACTTATGAC 1550
 DB 1407 CATGGGTTCTGCGCAGCTGCTGTCACCGAAGTCTGTTCTGCTACTGACTACTTATGAC 1466
 QY 1551 TTTGGAGAAGTTCTGCTGATGTTGTTCCCTTCAGTAACATTCGACTGGAAGAGCGCA 1610
 DB 1467 TTTGGAGAAGTTCTGCTGATGTTGTTCCCTTCAGTAACATTCGACTGGAAGAGCGCA 1526
 QY 1611 GACCTCAGTACCTCTATTTGCACTGATGAGGCGGATTTTAAATAGCTGAATTCATAT 1670
 DB 1527 GACCTCAGTACCTCTATTTGCACTGATGAGGCGGATTTTAAATAGCTGAATTCATAT 1586
 QY 1671 TTGGAATTAAGATTAATTTGGAACCTTTTATGGAATAATGAGATGATTTCCCACTTAA 1730

DB 1587 TTGGAATTAAGATTAATTTTGAACCTTTTATGGAATAATGAGATGATTTCCCACTTAA 1646
 QY 1721 TTATGACCAAAACAGAAATATTGGAAGCAAAAGGATTTCTTGGAAATTTTCTAGTGT 1790
 DB 1647 TTATGACCAAAACAGAAATATTGGAAGCAAAAGGATTTCTTGGAAATTTTCTAGTGT 1706
 QY 1791 GAACCTGCTGCTTTTCAATCATGATGTTTCCATATTAATGATCTGATCAATCA 1850
 DB 1707 GAACCTGCTGCTTTTCAATCATGATGTTTCCATATTAATGATCTGATCAATCA 1766
 QY 1851 AAAACCGCTTTCAGACCAAGAAATGTTTGGAAAGAGAGTGGCTGTTGC 1910
 DB 1767 AAAACCGCTTTCAGACCAAGAAATGTTTGGAAAGAGAGTGGCTGTTGC 1826
 QY 1911 AAATGTTTCTTTTATATGATGTTCTGATGATCCATCTGATGATTTGAT 1970
 DB 1827 AAATGTTTCTTTTATATGATGTTCTGATGATCCATCTGATGATTTGAT 1886
 QY 1971 TAAATTCCTTCCCTCTCCGGTGGAAATACCAACAATGATCTCTGATGAT 2030
 DB 1887 TAAATTCCTTCCCTCTCCGGTGGAAATACCAACAATGATCTCTGATGAT 1946
 QY 2031 TTTTTCCTTCAGTTAAAGTCTTGAATCCATCTCTATACCTCAACAACCT 2090
 DB 1947 TTTTTCCTTCAGTTAAAGTCTTGAATCCATCTCTATACCTCAACAACCT 2006
 QY 2091 TTTTGAAGCAAGTTGAACAGCTGCTGACCAACATGAGAGAAATCAATTTCAAAAT 2150
 DB 2007 TTTTGAAGCAAGTTGAACAGCTGCTGACCAACATGAGAGAAATCAATTTCAAAAT 2066
 QY 2151 TAAAAAAGATTTATCTACATGATGTTGATGATGAGAGCTCTCTCCCTGAAGT 2210
 DB 2067 TAAAAAAGATTTATCTACATGATGTTGATGATGAGAGCTCTCTCCCTGAAGT 2126
 QY 2211 TGGGTTTTGGAACAATAATACATTTGAGACAGATTAATGAACAGTTTCTAG 2265
 DB 2127 TGGGTTTTGGAACAATAATACATTTGAGACAGATTAATGAACAGTTTCTAG 2181

RESULT 7
 ABL40191
 ID ABL40191 standard; cDNA; 1545 BP.
 XX
 AC ABL40191;
 XX
 DT 23-MAY-2002 (first entry)
 XX
 DE Human G protein-coupled receptor TGR17-2 encoding cDNA SEQ ID NO:6.
 KW Human; G protein-coupled receptor; TGR17-2; neotropic; anti-inflammatory;
 KW vasotropic; immunomodulator; cytosolic; gene therapy; protein therapy;
 KW neurologic; inflammatory; circulatory; degenerative; immune system;
 KW digestive disease; cancer; gene; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key
 FT CDS 1..1545 Location/Qualifiers
 FT FT /*tag= a
 FT FT /partial
 FT FT /product= "TGR17-2"
 FT FT /note= "no stop codon given"
 XX
 PN MO200204640-A1.
 XX
 PD 17-JAN-2002.
 XX
 PF 06-JUL-2001, 2001WO-JP05878.
 XX
 PR 07-JUL-2000, 2000JP-0211989.
 XX
 PR 18-DEC-2000, 2000JP-0383794.
 XX

(TAKE) TAKEDA CHEM IND LTD.
 PA Moriya T, Ito T, Shintani Y, Miyajima N;
 XX WPI: 2002-179706/23.
 DR P-PSDB; ABB06251.
 XX G-protein coupled receptor protein TGR17 of human origin and DNA
 PT encoding it for diagnosis and treatment of cancer and circulatory and
 PT other diseases associated with its expression -
 XX
 PS Claim 7; Page 118-119; 145pp; Japanese.
 XX
 CC The present invention describes a human guanine nucleotide binding
 CC protein (G protein) coupled receptor protein designated TGR17, which has
 CC 5 variant forms (TGR17-1 to TGR17-5) of the receptor protein having
 CC additional residues at the N-terminal. The TGR17 proteins have nootropic,
 CC antiinflammatory, vasotropic, immunomodulator and cyclostatic activities.
 CC The TGR17 polynucleotides and protein can be used in gene therapy and
 CC protein therapy. G-protein coupled receptor proteins are cell membrane
 CC molecules mediating the cellular response to a large variety of signalling
 CC molecules. The TGR17 polynucleotides and proteins can be used in the
 CC diagnosis, treatment and prevention of diseases including neurological,
 CC inflammatory, circulatory and digestive diseases including neurodegenerative,
 CC diseases and cancer. The present sequence encodes human TGR17-2 from the
 CC present invention.
 CC
 SQ Sequence 1545 BP; 429 A; 320 C; 290 G; 506 T; 0 other;
 Query March 68.1%; Score 1543.4; DB 24; Length 1545;
 Basic Local Similarity 99.9%; Pred. No. 0;
 Matches 1544; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 718 ATGGTAAATACCTCTTGAAGCTCTTCCAGAGAGATGTGGCCAAATGCTCACTC 777
 Db 1 ATGGTAAATACCTCTTGAAGCTCTTCCAGAGAGATGTGGCCAAATGCTCACTC 60
 QY 778 AACTGGGTGATTTGGAAGGCAATAGAAATGATCTCACAAATTTCTGCTGCG 837
 Db 61 AACTGGGTGATTTGGAAGGCAATAGAAATGATCTCACAAATTTCTGCTGCG 120
 QY 838 TGGCAATTCGCTCAAGCTGCTTTCTGCTGGAATCAAAATGTTGTTGTTCCAGAGAG 897
 Db 121 TGGCAATTCGCTCAAGCTGCTTTCTGCTGGAATCAAAATGTTGTTGTTCCAGAGAG 180
 QY 898 ACATTTCTTCAATTAATAAATTTAGAGAGCTGATCTGTCTAGCAATAGATGAGAG 957
 Db 181 ACATTTCTTCAATTAATAAATTTAGAGAGCTGATCTGTCTAGCAATAGATGAGAG 240
 QY 958 CTATCACTCACTCTTTTAAAGACTTGAAGCTTCAAAAAGCTGAACCTGTCATCCAT 1017
 Db 241 CTATCACTCACTCTTTTAAAGACTTGAAGCTTCAAAAAGCTGAACCTGTCATCCAT 300
 QY 1018 CCTCTTAATGATCTTCCCAAGACAGTTGAAGCTTAAACCACTTCACTCTAGAC 1077
 Db 301 CCTCTTAATGATCTTCCCAAGACAGTTGAAGCTTAAACCACTTCACTCTAGAC 360
 QY 1078 CTGAAAGATAGATGATCCAAATATTAACACAGATGTTTCAACCATGAAAGATCTT 1137
 Db 361 CTGAAAGATAGATGATCCAAATATTAACACAGATGTTTCAACCATGAAAGATCTT 420
 QY 1138 TCTCAATTAATTTCAAAAATCTTGTGATCTGCTCTTCCCATGTCGAAATGT 1197
 Db 421 TCTCAATTAATTTCAAAAATCTTGTGATCTGCTCTTCCCATGTCGAAATGT 480
 QY 1198 ATGCCCTGAGGAGCGGATTTCTCAATTTAGAGACCTTGGCTAAACAATCTCTAGA 1257
 Db 481 ATGCCCTGAGGAGCGGATTTCTCAATTTAGAGACCTTGGCTAAACAATCTCTAGA 540
 QY 1258 ATATTTGTCTGGGTTATAGCTTCAATCTGCTTTGGAATCTTTTGTGATGGCAGT 1317
 Db 541 ATATTTGTCTGGGTTATAGCTTCAATCTGCTTTGGAATCTTTTGTGATGGCAGT 600

QY 1318 AGATCTTCAATTAAGCTGAATAATACAACTACGCTATGTCATCAAAATCTTTGTTGT 1377
 Db 601 AGATCTTCAATTAAGCTGAATAATACAACTACGCTATGTCATCAAAATCTTTGTTGT 660
 QY 1378 GCTGATTCCTGATGGGTGTTTACTGTTCTTTGTTGGCAATTTTGCATTAATAATCCGA 1437
 Db 661 GCTGATTCCTGATGGGTGTTTACTGTTCTTTGTTGGCAATTTTGCATTAATAATCCGA 720
 QY 1438 GGGCAGATCAGAGATAGCTGCTGCTGTGATGAGAGCGTGCAGNCCGCTCATGGGG 1497
 Db 721 GGGCAGATCAGAGATAGCTGCTGCTGTGATGAGAGCGTGCAGNCCGCTCATGGGG 780
 QY 1498 TTCTGCGCATGCTGTCACAGAGTCTGTTCTGCTACTGACTTGAATTTGATGGAG 1557
 Db 781 TTCTGCGCATGCTGTCACAGAGTCTGTTCTGCTACTGACTTGAATTTGATGGAG 840
 QY 1558 AAGTTCCTGGTCAATGTTGTTCCCTTTAGTAACTTGAACCTGGAACCGCAGACTCA 1617
 Db 841 AAGTTCCTGGTCAATGTTGTTCCCTTTAGTAACTTGAACCTGGAACCGCAGACTCA 900
 QY 1618 GTCACTCTCATTTGCAATGATGAGGAGGATTTTAAATAGCTGTAATTTCAATTTGGAAT 1677
 Db 901 GTCACTCTCATTTGCAATGATGAGGAGGATTTTAAATAGCTGTAATTTCAATTTGGAAT 960
 QY 1678 AAGGATTAATTTGGAACCTTTTATGGAATAATGAGATGTTTCCACTTTATATGAC 1737
 Db 961 AAGGATTAATTTGGAACCTTTTATGGAATAATGAGATGTTTCCACTTTATATGAC 1020
 QY 1738 CAAACAGAAATATTTGGAACCAAGGATTTCTTGGAAATTTTCCATGAGTGAACCTTG 1797
 Db 1021 CAAACAGAAATATTTGGAACCAAGGATTTCTTGGAAATTTTCCATGAGTGAACCTTG 1080
 QY 1798 CTGGCTTTTCTCATCATTTGTTGTTTCTTATATTAATGTTCTGTTTCATTTCAAAAACC 1857
 Db 1081 CTGGCTTTTCTCATCATTTGTTGTTTCTTATATTAATGTTCTGTTTCATTTCAAAAACC 1140
 QY 1858 GCCTTGCAACAACAAGATGAGAAATGTTTGGAAAGAGAGGTGCTGTGCAATCGT 1917
 Db 1141 GCCTTGCAACAACAAGATGAGAAATGTTTGGAAAGAGAGGTGCTGTGCAATCGT 1200
 QY 1918 TTCTTTTATATAGTGTCTGATGCGCATCTGCTGATTTCTGTAATTTGTAATTAATC 1977
 Db 1201 TTCTTTTATATAGTGTCTGATGCGCATCTGCTGATTTCTGTAATTTGTAATTAATC 1260
 QY 1978 CTTTCCCTCTCCGGGGGAAATACAGACACATGACTTCTGATGATGATTTTTC 2037
 Db 1261 CTTTCCCTCTCTCCGGGGGAAATACAGACACATGACTTCTGATGATGATTTTTC 1320
 QY 2038 CTTCAGTTAAACAGTGTGTAATTCATCTCTTATCTCTCAACCAACTTTTAAAG 2097
 Db 1321 CTTCAGTTAAACAGTGTGTAATTCATCTCTTATCTCTCAACCAACTTTTAAAG 1380
 QY 2098 GACAAAGTTGAAACAGCTGCTGCAACCAATCAGAGAAATCAATTTTCAAAATTAATAA 2157
 Db 1381 GACAAAGTTGAAACAGCTGCTGCAACCAATCAGAGAAATCAATTTTCAAAATTAATAA 1440
 QY 2158 AAAAGTTATCTATCATCATTTGTTGATAGAGACTCTTCCCTGAAACTTGAGGTT 2217
 Db 1441 AAAAGTTATCTATCATCATTTGTTGATAGAGACTCTTCCCTGAAACTTGAGGTT 1500
 QY 2218 TTGAACAAATTAACACTTGGAGACAGTATATGAAACCAAGTTTC 2262
 Db 1501 TTGAACAAATTAACACTTGGAGACAGTATATGAAACCAAGTTTC 1545
 RESULT 8
 ABL40192
 ID ABL40192 standard; cDNA; 1473 BP.
 XX
 AC ABL40192;
 XX
 DT 23-MAY-2002 (first entry)
 XX

QY 2038 CTTCAGTTAAGAGTCTTGTATGATCAATCCTCTAATCTACAGACCACTTTTAAAG 2097
 DB 1249 CTTCCAGTTAAGAGTCTTGTATGATCAATCCTCTAATCTACAGACCACTTTTAAAG 1368
 QY 2098 GACAAAGTTGAAACAGCTGCTGCAACAAATCAAGGAAATCAATTTCAAAATTTAAAAA 2157
 DB 1309 GACAAAGTTGAAACAGCTGCTGCAACAAATCAAGGAAATCAATTTCAAAATTTAAAAA 1368
 QY 2158 AAAAGTTATCTACATTCATTTGTGATGATAGAGACTCTCTCCCTGAACTGGGGGT 2217
 DB 1369 AAAAGTTATCTACATTCATTTGTGATGATAGAGACTCTCTCTCCCTGAACTGGGGGT 1428
 QY 2218 TTGAACAAATATACACTTGAGAGACAGTATTAATGAACCAATTTCC 2262
 DB 1429 TTGAACAAATATACACTTGAGAGACAGTATTAATGAACCAATTTCC 1473

RESULT 9
 ABL40188
 ID ABL40188 standard; cDNA; 1830 BP.
 AC ABL40188;
 XX
 DT 23-MAY-2002 (first entry)
 DE Human G protein-coupled receptor TGR17-1 encoding cDNA SEQ ID NO:2.
 XX
 KW Human; G protein-coupled receptor; TGR17-1; nocotropic; antiinflammatory;
 KW vasotropic; immunomodulator; cytoprotatic; gene therapy; protein therapy;
 KW neurological; inflammatory; circulatory; degenerative; immune system;
 KW digestive disease; cancer; gene; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..1830
 FT /tag= a
 FT /partial
 FT /product= "TGR17-1"
 FT /note= "no stop codon given"
 XX
 PN WO200204640-A1.
 PD 17-JAN-2002.
 PF 06-JUL-2001; 2001WO-0P05878.
 PR 07-JUL-2000; 2000JP-0211989.
 PR 18-DEC-2000; 2000JP-0383794.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 PI Moriya T, Ito T, Shintani Y, Miyajima N;
 DR WPI: 2002-179706/23.
 DR P-PSDB; ABB06250.
 PT G-protein coupled receptor protein TGR17 of human origin and DNA
 PT encoding it for diagnosis and treatment of cancer and circulatory and
 PT other diseases associated with its expression -
 XX
 PS Claim 7, Page 114-115; 145pp; Japanese.
 CC The present invention describes a human guanine nucleotide binding
 CC protein (G protein) coupled receptor protein designated TGR17, which has
 CC 5 variant forms (TGR17-1 to TGR17-5) of the receptor protein having
 CC additional residues at the N-terminal. The TGR17 proteins have nocotropic,
 CC antiinflammatory, vasotropic, immunomodulator and cytoprotatic activities.
 CC The TGR17 polynucleotides and protein can be used in gene therapy and
 CC protein therapy. G-protein coupled receptor proteins are cell membrane
 CC proteins mediating the cellular response to a large variety of signalling
 CC molecules. The TGR17 polynucleotides and proteins can be used in the
 CC diagnosis, treatment and prevention of diseases including neurological,

CC inflammatory, circulatory, degenerative, immune system and digestive
 CC diseases and cancer. The present sequence encodes human TGR17-1 from the
 CC present invention.
 XX
 SQ Sequence 1830 BP; 516 A; 377 C; 351 G; 586 T; 0 other;
 Query Match 61.1%; Score 1384.8; DB 24; Length 1830;
 Best Local Similarity 80.8%; Pred. No. 0;
 Matches 1828; Conservative 0; Mismatches 2; Indels 432; Gaps 1;
 QY 1 ATGATGTTTCTTCTGTTTAAACATCTCTTCCCTGCGGAACTTACCAAGTCTTCC 60
 DB 1 ATGATGTTTCTTCTGTTTAAACATCTCTTCCCTGCGGAACTTACCAAGTCTTCC 60
 QY 61 CTACTGATTTCACTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 120
 DB 61 CTACTGATTTCACTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 120
 QY 121 ATCACTCTTCATGCGCAAAAAGATATTTTCCCTGCGGAACTTACCAAGTCTTCC 180
 DB 121 ATCACTCTTCATGCGCAAAAAGATATTTTCCCTGCGGAACTTACCAAGTCTTCC 180
 QY 181 CGAGCTTTTCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 240
 DB 181 CGAGCTTTTCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 240
 QY 241 GGTGACACTAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 300
 DB 241 GGTGACACTAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 300
 QY 241 GGTGACACTAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 300
 DB 241 GGTGACACTAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 300
 QY 301 GCCTTAAACACAGAGTCTTCTTAAACAGATATCAATGCTGACTGCAAGAAACT 360
 DB 301 GCCTTAAACACAGAGTCTTCTTAAACAGATATCAATGCTGACTGCAAGAAACT 360
 QY 361 GAATTTGAAATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
 DB 361 GAATTTGAAATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
 QY 421 TTACTGCTCTTAAAGAAACAAATCAAGTCTTCCAGATTAAGTTTCAATCAATAC 480
 DB 421 TTACTGCTCTTAAAGAAACAAATCAAGTCTTCCAGATTAAGTTTCAATCAATAC 480
 QY 481 ACAAACTTAAAGATATTTCTTCAAGATTAATGCAATTGACATATCCAGAGAAACA 540
 DB 481 ACAAACTTAAAGATATTTCTTCAAGATTAATGCAATTGACATATCCAGAGAAACA 540
 QY 541 TTTTGTGATTAATGATCTGCAATATATATCTCAACCAACTGATCACAACCTC 600
 DB 541 TTTTGTGATTAATGATCTGCAATATATATCTCAACCAACTGATCACAACCTC 600
 QY 601 AGACCTGATATTCAAAGACTTACATCAGCTAATCTGATATCTAGATGACATCA 660
 DB 601 AGACCTGATATTCAAAGACTTACATCAGCTAATCTGATATCTAGATGACATCA 660
 QY 661 ATTAACGAATTTGACAGCGCTGTTTACGGGATTAATCTTGTCTTCTGCTATG 720
 DB 661 ATTAACGAATTTGACAGCGCTGTTTACGGGATTAATCTTGTCTTCTGCTATG 720
 QY 721 GTTATTAATCTAGTAAGCTCTTCCCAAGAGATGTGTGCCAATGCTCAACTCAAC 780
 DB 721 GTTATTAATCTAGTAAGCTCTTCCCAAGAGATGTGTGCCAATGCTCAACTCAAC 780
 QY 781 TGGGTGATTTGAAAGCAATAGATTAATAGATCTCACAATTTCTAGCTGTG 840
 DB 781 TGGGTGATTTGAAAGCAATAGATTAATAGATCTCACAATTTCTAGCTGTG 840
 QY 841 GATTCGCTCACAGTGTGTTTCTGCTTGAATAATGATGTTTGTTCAGAGAGACA 900
 DB 841 GATTCGCTCACAGTGTGTTTCTGCTTGAATAATGATGTTTGTTCAGAGAGACA 900
 QY 901 TTTTCTTATTAATAAATTTAGAGAACTGATCTGTACCAATAGATAGAGAGCTA 960
 DB 901 TTTTCTTATTAATAAATTTAGAGAACTGATCTGTACCAATAGATAGAGAGCTA 960
 QY 961 TGGATCTGTACCAATAGATAGAGAGCTA 528
 DB 961 TGGATCTGTACCAATAGATAGAGAGCTA 528

QY 961 TCACCTCACTTTTAAAGCTTGAAGCTTCTACAAAGCTGAACCTGTCATCCAACTCT 1020
 DB 529 TCACCTCACTTTTAAAGCTTGAAGCTTCTACAAAGCTGAACCTGTCATCCAACTCT 588
 QY 1021 CTTATGATCTTCAAGAAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTT 1080
 DB 589 CTTATGATCTTCAAGAAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTT 648
 QY 1081 GAAAGATGAGATTCCTCAATATTAACACAGATGTTTCAACCCATGAAGATCTTCT 1140
 DB 649 GAAAGATGAGATTCCTCAATATTAACACAGATGTTTCAACCCATGAAGATCTTCT 708
 QY 1141 CACATTTATTTCAAAAACCTTGTGATCTGCTCTATGCTCCCATGCTCCGATATGTATG 1200
 DB 709 CACATTTATTTCAAAAACCTTGTGATCTGCTCTATGCTCCCATGCTCCGATATGTATG 768
 QY 1201 CCCTTGACGAGCGGATTTCTTCAATTTGAAGACCTCTTGAGCTAACAATCTCTGAGATA 1260
 DB 769 CCCTTGACGAGCGGATTTCTTCAATTTGAAGACCTCTTGAGCTAACAATCTCTGAGATA 828
 QY 1261 TTTGCTGGGTTATAGCTTTCATTTACCTGCTTGAAGATCTTTTGTCAATGGCATGAGA 1320
 DB 829 TTTGCTGGGTTATAGCTTTCATTTACCTGCTTGAAGATCTTTTGTCAATGGCATGAGA 888
 QY 1321 TCTTTTATTAAGCTGAATAATCACTCAAGCTATGCTCAATCAAAATCTTTGTGTGCT 1380
 DB 889 TCTTTTATTAAGCTGAATAATCACTCAAGCTATGCTCAATCAAAATCTTTGTGTGCT 948
 QY 1381 GATTCGCTGATGGGTTTACTGTTCTTGTGGAATTTTGAATTTTGAATTTTGAATTTTGA 1440
 DB 949 GATTCGCTGATGGGTTTACTGTTCTTGTGGAATTTTGAATTTTGAATTTTGAATTTTGA 1008
 QY 1441 CAGTATCAGAAATGATCTTGTGCTGATGAGAGAGGCTGAGCTGCTGATGGGCTTC 1500
 DB 1009 CAGTATCAGAAATGATCTTGTGCTGATGAGAGAGGCTGAGCTGCTGATGGGCTTC 1068
 QY 1501 CTGGCCATGCTGCAACCGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560
 DB 1069 CTGGCCATGCTGCAACCGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1128
 QY 1561 TTCCTGATCTTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1620
 DB 1129 TTCCTGATCTTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1188
 QY 1621 ATCTCATTTGCAATCTGATGAGGAGGATTTTAAATGCTGTAATTCATTTTGAATTAAG 1680
 DB 1189 ATCTCATTTGCAATCTGATGAGGAGGATTTTAAATGCTGTAATTCATTTTGAATTAAG 1248
 QY 1681 GATTAATTTGGAACCTTTTATGGAATAATGGAATGTTTCCCACTTTTATGACCA 1740
 DB 1249 GATTAATTTGGAACCTTTTATGGAATAATGGAATGTTTCCCACTTTTATGACCA 1308
 QY 1741 ACAGAAATATTTGAACCAAGGATTTCTTGAATTTTCTTGAATTTTGAATTTTGAATTTG 1800
 DB 1309 ACAGAAATATTTGAACCAAGGATTTCTTGAATTTTCTTGAATTTTGAATTTTGAATTTG 1368
 QY 1801 GCTTTTCTCATTTGTTGTTTCTTATATTAATGTTTCTTCTTCTTCTTCTTCTTCTTCT 1860
 DB 1369 GCTTTTCTCATTTGTTGTTTCTTATATTAATGTTTCTTCTTCTTCTTCTTCTTCTTCT 1428
 QY 1861 TTGACAGCAACAGAAATGGAATTTGTTTGAAGAGAGGCTGTTTGAAGATTCGTTTC 1920
 DB 1429 TTGACAGCAACAGAAATGGAATTTGTTTGAAGAGAGGCTGTTTGAAGATTCGTTTC 1488
 QY 1921 TTTTATTAAGTGTCTGATGCTGCTGATGCTGCTGATGCTGCTGATGCTGCTGATGCTGCT 1980
 DB 1489 TTTTATTAAGTGTCTGATGCTGCTGATGCTGCTGATGCTGCTGATGCTGCTGATGCTGCT 1548
 QY 1981 TCCCTCTTCCGGGATGGAATTAACAGACATGCTTCTGATGATGATTTTCTTCTTCTTCT 2040
 DB 1549 TCCCTCTTCCGGGATGGAATTAACAGACATGCTTCTGATGATGATTTTCTTCTTCTTCT 1608

QY 2041 CCAGTTAACAGTGTCTTGAATTCATCTCTTATCTCTACAACTTTTAAAGAC 2100
 DB 1609 CCAGTTAACAGTGTCTTGAATTCATCTCTTATCTCTACAACTTTTAAAGAC 1668
 QY 2101 AAGTTGAACAGCTGCTGACAAACATCAGAGGAATCAATTTTCAAAATTTAAAAA 2160
 DB 1669 AAGTTGAACAGCTGCTGACAAACATCAGAGGAATCAATTTTCAAAATTTAAAAA 1728
 QY 2161 AGTTATCTACATCTTGTGTGATGATGAGACTCTTCTTCCCTGAAATCTGGGTTTGG 2220
 DB 1729 AGTTATCTACATCTTGTGTGATGATGAGACTCTTCTTCCCTGAAATCTGGGTTTGG 1788
 QY 2221 AACAAATTAACCTTGAGACAGTATTAATGAACAGTTTCC 2262
 DB 1789 AACAAATTAACCTTGAGACAGTATTAATGAACAGTTTCC 1830

RESULT 10
 ABR33349
 ID ABR33349 standard, DNA, 1121 BP.
 XX
 AC ABR33349;
 XX
 DT 22-MAY-2003 (first entry)
 XX
 DE NOVX DNA sequence SEQ ID NO 13.
 XX
 XX Hepatotropic; immunosuppressive; cardiant; hypertensive; tranquilizer;
 XX antiparasitic; antibacterial; protozoicide; fungicide; nootropic;
 XX antiparasitic; neuroprotective; cerebroprotective; antiparkinsonian;
 XX anticonvulsant; antidiabetic; analgesic; dermatological; keratolytic;
 XX antiseborrheic; antihemetic; anticholinergic; antiinflammatory; anti-HIV;
 XX cytotaxic; antiaesthetic; antipruritic; hypotensive; osteopathic;
 XX antileptic; anorectic; antidiabetic; antiallergic; haemostatic;
 XX neuroleptic; antidepressant; antifertility; NOVX; human disease;
 XX NOVX-associated disorder; trauma; viral; bacterial; fungal; protozoal;
 XX parasitic infection; Alzheimer's disease; stroke; forensic biology;
 XX immunogen; non-human transgenic animal; gene therapy; gene; de.
 OS Unidentified.
 XX
 PN WO200281517-A2.
 XX
 PD 17-OCT-2002.
 XX
 XX
 PF 22-JAN-2002; 2002WO-US02064.
 XX
 XX 19-JAN-2001; 2001US-262892P.
 PR 23-JAN-2001; 2001US-263598P.
 PR 24-JAN-2001; 2001US-263799P.
 PR 25-JAN-2001; 2001US-264117P.
 PR 25-JAN-2001; 2001US-264139P.
 PR 26-JAN-2001; 2001US-264478P.
 PR 30-JAN-2001; 2001US-263531P.
 PR 02-MAR-2001; 2001US-272870P.
 PR 14-MAR-2001; 2001US-275927P.
 PR 14-MAR-2001; 2001US-275990P.
 PR 15-MAR-2001; 2001US-276449P.
 PR 20-MAR-2001; 2001US-277358P.
 PR 23-MAR-2001; 2001US-278151P.
 PR 29-MAR-2001; 2001US-279857P.
 PR 20-APR-2001; 2001US-285140P.
 PR 20-APR-2001; 2001US-285141P.
 PR 30-APR-2001; 2001US-287484P.
 PR 17-MAY-2001; 2001US-281701P.
 PR 08-JUN-2001; 2001US-289606P.
 PR 10-JUL-2001; 2001US-304353P.
 PR 10-JUL-2001; 2001US-304355P.
 PR 12-JUL-2001; 2001US-304886P.
 PR 09-AUG-2001; 2001US-311289P.
 PR 13-AUG-2001; 2001US-311975P.
 PR 16-AUG-2001; 2001US-312937P.
 PR 18-OCT-2001; 2001US-350227P.

PR 29-NOV-2001; 2001US-334198P.
 XX (CUBA-) CUBAGEN CORP.
 XX
 P1 Deciolefofiro MF, Padigaru M, Miller C, Tchernev V, Zhong H;
 P1 Zhong M, Anderson D, Ballinger R, Gerlach V, Spletok KA;
 P1 Rastelli L, Kekuda R, Guo X, Zehusen B, Andrew A, Baumgartner J;
 P1 Paturjan M, Burgess CE, Eisen A, Wolenc A, Baumgartner J;
 P1 Shinkens RA, Guev V, Vernet CM, Taubier RJ, Pena C, Shenoy S;
 P1 Li L, Caeman S, Boldog F, Fernandes E, Smithson G, Malyankar U;
 P1 Tallon B, Liu X;
 XX MPI; 2003-058504/05.
 DR P-PSDB; AB337884.
 XX
 PT New polypeptides, designated as NOX, useful for diagnosing and
 PT treating infections, neurological diseases, cancer, allergy, and bone,
 PT immunological, skin, renal, brain, muscle and autoimmune disorders -
 XX
 PS Claim 9; Page 58; 672pp; English.
 XX
 CC The invention relates to a novel isolated polypeptide, designated NOX
 CC (NOV1 - 33), consisting of a mature form of one of 61 sequences, given
 CC in the specification, or its variant, where amino acid residue(s) in the
 CC variant differ from the mature form, provided that the variant differs
 CC in not more than 15 % of the amino acids from the sequence of the mature
 CC form. The NOV polypeptides, nucleic acids encoding the polypeptides, and
 CC an antibody to the polypeptides, are useful for treating or preventing a
 CC NOX-associated disorder (NOX-associated disorder). NOX polypeptides and
 CC with a human disease (NOX-associated disorder). NOX polypeptides and
 CC the encoding nucleic acids, are useful for determining the presence of or
 CC predisposition to a disease associated with altered levels of NOX
 CC polypeptide and polynucleotide, by measuring the level of polypeptide
 CC expression or the amount of nucleic acid from a mammal and comparing it
 CC with another mammal not having or not predisposed to the disease. NOX
 CC polypeptide is also useful for identifying an agent that binds to NOX
 CC and a cell expressing NOX is useful for identifying an agent that
 CC modulates the expression or activity of NOX. The antibodies and a
 CC polypeptide having 95 % sequence identity to NOX polypeptides are also
 CC useful for treating a pathological state in a mammal. The antibodies are also
 CC useful for determining the presence or amount of NOX in a sample. NOX
 CC polypeptides, polynucleotides and antibodies specific for the
 CC polypeptides are useful for treating or preventing disorders or syndromes
 CC including trauma, viral, bacterial, fungal, protozoal, and parasitic
 CC infections. They can also treat disorders such as e.g., Alzheimer's
 CC disease or a stroke. The NOV encoding nucleic acids are useful for
 CC expressing the NOV proteins, to detect NOV mRNA, or a genetic lesion in
 CC a NOV gene and to modulate NOV activity. NOV sequences are also useful
 CC for identifying a cell or tissue type in a biological sample, to amplify
 CC DNA sequences from very small biological samples such as tissues e.g.,
 CC hair or skin or body fluids in forensic biology and as primers and probes
 CC for use in identifying and/or cloning NOV homologues in other cell
 CC types. The NOV proteins are useful as an immunogen to generate
 CC antibodies which are useful for diagnostically monitoring protein levels
 CC and modulating NOV activity. Cells comprising NOV nucleic acids are
 CC useful for producing non-human transgenic animals which are useful for
 CC studying the function and/or activity of NOV protein and for identifying
 CC and/or evaluating modulators of NOV protein activity. The NOV nucleic
 CC acids can be used in gene therapy. This polynucleotide sequence
 CC represents a NOV DNA sequence of the invention.
 XX
 SQ Sequence 1121 BP; 289 A; 228 C; 222 G; 382 T; 0 other;
 Query Match 48.8%; Score 1105.8; DB 25; Length 1121;
 Best Local Similarity 99.7%; Pred. No. 1.4e-285;
 Matches 1118; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
 QY 1146 TTAATTCAGAAAGCTTCTGATGCTCTCTAT-GCTCCCATGTCGGAATATGATGCTCT 1204
 DB 1 TTAATTCAGAAAGCTTCTGATGCTCTCTATGCTCTCTATGCTCTCTATGCTCTCTATGCTCT 60
 QY 1205 TACGAGCGGCAATTTCTTATTTAGAGACTCTTGCTTAACATATCTCTCAAAATTTTG 1264

DB 61 TGACGAGCGGCAATTTCTTATTTAGAGACTCTTGCTTAACATATCTCTCAAAATTTTG 120
 QY 1265 TCGGGTTATAGCTTTTATTAACCTGCTTGGAAATCTTTTGTGATGGCATGATCTT 1324
 DB 121 TCTGGTTATAGCTTTTATTAACCTGCTTGGAAATCTTTTGTGATGGCATGATCTT 180
 QY 1325 TCATTAAGCTGAAATATCACTGACCTATGTCATCAAAATCTTTGTGCTGATTT 1384
 DB 181 TCATTAAGCTGAAATATCACTGACCTATGTCATCAAAATCTTTGTGCTGATTT 240
 QY 1385 GCTGATGGGTGTTTACTGTTCTTTGTGAGCAATTTTGATATAAATCCGAGGCGAGT 1444
 DB 241 GCTGATGGGTGTTTACTGTTCTTTGTGAGCAATTTTGATATAAATCCGAGGCGAGT 300
 QY 1445 ATCAGAGTATGCTTCTGATGATGAGAGCGGAGTCCGCTCATGGGTTCTCGG 1504
 DB 301 ATCAGAGTATGCTTCTGATGATGAGAGCGGAGTCCGCTCATGGGTTCTCGG 360
 QY 1505 CCATGCTGTCCACGGAAGTCTCTGCTGCTACTGACCTACTGATCTTGGAGAGTTCC 1564
 DB 361 CCATGCTGTCCACGGAAGTCTCTGCTGCTACTGACCTACTGATCTTGGAGAGTTCC 420
 QY 1565 TGTGATTTGTTTCCCTTCACTGATCACTGACCTGGAAGAGGAGCTGATCTC 1624
 DB 421 TGTGATTTGTTTCCCTTCACTGATCACTGACCTGGAAGAGGAGCTGATCTC 480
 QY 1625 TCATTTGATGATGAGGCGGAGATTTTATAGCTGATATCCATTTTGAATAGAGAT 1684
 DB 481 TCATTTGATGATGAGGCGGAGATTTTATAGCTGATATCCATTTTGAATAGAGAT 540
 QY 1685 ATTTTGAAGCTTTTATAGGAAAAATGAGATATTTTCCACTTATATAGCAAAAG 1744
 DB 541 ATTTTGAAGCTTTTATAGGAAAAATGAGATATTTTCCACTTATATAGCAAAAG 600
 QY 1745 AAGATATGGAAGCAAGAGGATTTCTTGGAAATTTTCTAGGTGATCTGCTGCTT 1804
 DB 601 AAGATATGGAAGCAAGAGGATTTCTTGGAAATTTTCTAGGTGATCTGCTGCTT 660
 QY 1805 TTTCATCATGTTGTTTCTCTATATCTATGTTCTGTTCAATCAAAACCGCTTGC 1864
 DB 661 TTTCATCATGTTGTTTCTCTATATCTATGTTCTGTTCAATCAAAACCGCTTGC 720
 QY 1865 AGACCAAGAAATGAGAAATTTTGGAGAGAGGTGCTTGGAAATGCTTTCTTT 1924
 DB 721 AGACCAAGAAATGAGAAATTTTGGAGAGAGGTGCTTGGAAATGCTTTCTTT 780
 QY 1925 TTATAGTGTCTCTGATGCTCTGCTGCTGATTTCTCTATATTTGATTAATCTTTCC 1984
 DB 781 TTATAGTGTCTCTGATGCTCTGCTGCTGATTTCTCTATATTTGATTAATCTTTCC 840
 QY 1985 TCTTCCGGGTGGAATATCAAGACAAATGACTTCCGTGATAGTATTTTTCCTTCAG 2044
 DB 841 TCTTCCGGGTGGAATATCAAGACAAATGACTTCCGTGATAGTATTTTTCCTTCAG 900
 QY 2045 TTAACAGTCTTGAATCAATCTCTATATCTCTCAACCAACTTTTAAAGCAAGT 2104
 DB 901 TTAACAGTCTTGAATCAATCTCTATATCTCTCAACCAACTTTTAAAGCAAGT 960
 QY 2105 TGAACAGCTCTGCAAAATCAAGAGGAATATTTTCAAAATTTAAAAAATTT 2164
 DB 961 TGAACAGCTCTGCAAAATCAAGAGGAATATTTTCAAAATTTAAAAAATTT 1020
 QY 2165 TATCTACATCATGTTGTGATGATGAGAGCTCTCTCTGAAACTTGGGGTTTGAACA 2224
 DB 1021 TATCTACATCATGTTGTGATGATGAGAGCTCTCTCTGAAACTTGGGGTTTGAACA 1080
 QY 2225 AAATTAACCTTGAAGACAGTATTAATGAACCAATTTTCTAG 2285
 DB 1081 AAATTAACCTTGAAGACAGTATTAATGAACCAATTTTCTAG 1121

RESULT 11
 AAS07943

ID AAS07943 standard; cDNA; 1068 BP.
AC AAS07943;
XX
DT 23-OCT-2001 (first entry)
XX
DE Human cDNA encoding G-protein coupled receptor, hrup16.
XX
KW Human; G-protein coupled receptor; GPCR; hrup16; agonist;
XX Inverse agonist; lung cancer; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..1068
FT /*tag= a
FT /product= "hrup16"
XX
PN M0200136471-A2.
XX
PD 25-MAY-2001.
XX
PF 16-NOV-2000; 2000MO-US31509.
XX
PR 17-NOV-1999; 99US-0166088.
XX 17-NOV-1999; 99US-0166099.
XX 17-NOV-1999; 99US-0166369.
XX 23-DEC-1999; 99US-0171900.
XX 23-DEC-1999; 99US-0171901.
XX 23-DEC-1999; 99US-0171902.
XX 11-FEB-2000; 2000US-0181749.
XX 14-MAR-2000; 2000US-0189258.
XX 14-MAR-2000; 2000US-0189259.
XX 10-APR-2000; 2000US-0195898.
XX 10-APR-2000; 2000US-0195899.
XX 10-APR-2000; 2000US-0196078.
XX 28-APR-2000; 2000US-0200419.
XX 12-MAY-2000; 2000US-0203630.
XX 12-JUN-2000; 2000US-0210741.
XX 12-JUN-2000; 2000US-0210982.
XX 21-AUG-2000; 2000US-0226760.
XX 26-SEP-2000; 2000US-0235418.
XX 26-SEP-2000; 2000US-0235779.
XX 20-OCT-2000; 2000US-0242332.
XX 20-OCT-2000; 2000US-0242343.
XX
PA (AREN-) ARENA PHARM INC.
XX
PI Chen R, Dang HT, Lowitz KP;
XX
DR WPI; 2001-355616/37.
XX
DR P-PSDB; AAU04370.
XX
PT Endogenous and non-endogenous versions of human G-protein coupled
PT receptors for direct identification of candidate compounds as agonists,
PT inverse agonists or partial agonists for use as therapeutic agents -
XX
PS Claim 35; Page 104-105; 159pp; English.
XX
XX The sequence encodes a human G-protein coupled receptor (GPCR),
CC hrup16. The endogenous and non-endogenous, constitutively activated
CC versions of human G-protein coupled receptors (GPCR) are useful for
CC direct identification of candidate compounds as receptor agonists,
CC inverse agonists or partial agonists having applicability as therapeutic
CC agents for treating diseases related to GPCR, e.g. lung cancer.
CC Non-endogenous version of human GPCRs are also utilized in research
CC settings and in vitro and in vivo system, incorporating GPCRs can be
CC utilized to elucidate and understand the roles these receptors
CC play in the human condition, both normal and diseased.
XX
SQ Sequence 1068 BP; 278 A; 215 C; 214 G; 361 T; 0 other;
Query Match 47.1%; Score 1066.4; DB 22; Length 1068;

Best Local Similarity 99.9%; Pred. No. 4,9e-275;
Matches 1067; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1198 ATGCCCTTGACGAGCGCATTTCTTCATTGAGACCTCTGGCTAACAAATTCCTCAGA 1257
DB 1 ATGCCCTTGACGAGCGCATTTCTTCATTGAGACCTCTGGCTAACAAATTCCTCAGA 60
QY 1258 ATATTGCTGGGTTATAGCTTTCATTACCTGCTTGGAAATCTTTTGTCAATGGCAG 1317
DB 61 ATATTGCTGGGTTATAGCTTTCATTACCTGCTTGGAAATCTTTTGTCAATGGCAG 120
QY 1318 AGATCTTTCATTAAAGCTGAAATCAACTCAGCTATGCTCATCAAAATCTTTGTTGT 1377
DB 121 AGATCTTTCATTAAAGCTGAAATCAACTCAGCTATGCTCATCAAAATCTTTGTTGT 180
QY 1378 GCTGATGCTGATGGGTTTACTGTTCTTTGTTGGCATTTGGATTAATAATACCA 1437
DB 181 GCTGATGCTGATGGGTTTACTGTTCTTTGTTGGCATTTGGATTAATAATACCA 240
QY 1438 GGGCAGTATCAGAGTATGCTTGTCTGTGTGAGAGAGCGTGCATGCGCTCATGGG 1497
DB 241 GGGCAGTATCAGAGTATGCTTGTCTGTGTGAGAGAGCGTGCATGCGCTCATGGG 300
QY 1498 TTCTGGGCGATGCTGTCCACGGAAGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 1557
DB 301 TTCTGGGCGATGCTGTCCACGGAAGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 360
QY 1558 AAGTCTCTGATGATGTTCTTCCCTTCAGTAACTTGCACCTGGAAGCGGACCTCA 1617
DB 361 AAGTCTCTGATGATGTTCTTCCCTTCAGTAACTTGCACCTGGAAGCGGACCTCA 420
QY 1618 GTTCATCTCATTTGTCATCTGATGCGGGGATTTTATAGCTGTATTCATTTGGAT 1677
DB 421 GTTCATCTCATTTGTCATCTGATGCGGGGATTTTATAGCTGTATTCATTTGGAT 480
QY 1678 AAGATTAATTTTGGAACTTTATGAGGAAATGAGTATGTTTCCCACTTATTTATGAC 1737
DB 481 AAGATTAATTTTGGAACTTTATGAGGAAATGAGTATGTTTCCCACTTATTTATGAC 540
QY 1738 CAACAGAAAGATTTGGAACAAAGGATATCTCTTGAATTTTCTAGGTGTGAACCTTG 1797
DB 541 CAACAGAAAGATTTGGAACAAAGGATATCTCTTGAATTTTCTAGGTGTGAACCTTG 600
QY 1798 CTGGCTTCTCATCATCTGATGTTTCTTCTATTAATGATGCTGCTCAATCAAAAC 1857
DB 601 CTGGCTTCTCATCATCTGATGTTTCTTCTATTAATGATGCTGCTCAATCAAAAC 660
QY 1858 GCCTTGACAGCAAGAAATGAAGATTTGTTGGAAGAGGTGCTGTGCAATCGT 1917
DB 661 GCCTTGACAGCAAGAAATGAAGATTTGTTGGAAGAGGTGCTGTGCAATCGT 720
QY 1918 TTCTTTTATATAGTGTCTGTGATGCTGCTGATGCTGTGATTTGATTTAAATC 1977
DB 721 TTCTTTTATATAGTGTCTGTGATGCTGCTGATGCTGTGATTTGATTTAAATC 780
QY 1978 CTTCCTCTCTCCGGTGAATATACAGACAAATGCTCTGATAGATTTTTC 2037
DB 781 CTTCCTCTCTCCGGTGAATATACAGACAAATGCTCTGATAGATTTTTC 840
QY 2038 CTTCAGTTAAGAGTCTTGAATCAATCTCTATACTCTGACAAACCACTTTTAAAG 2097
DB 841 CTTCAGTTAAGAGTCTTGAATCAATCTCTATACTCTGACAAACCACTTTTAAAG 900
QY 2098 GACAAATTGAACAGTCTGTGCAAAACATCAGAGGAATCAATTTTCAAAATTAATAA 2157
DB 901 GACAAATTGAACAGTCTGTGCAAAACATCAGAGGAATCAATTTTCAAAATTAATAA 960
QY 2158 AAAAGTTATCTACATCAATGATGAGATGAGAGACTCTCTCCCTGAACCTTGGGGTT 2217
DB 961 AAAAGTTATCTACATCAATGATGAGATGAGAGACTCTCTCCCTGAACCTTGGGGTT 1020
QY 2218 TTGAACAAATAACACTTGGAGACAGTATTAAGAAACAGTTTCTTGA 2265

Db 1021 TTGAACAAATTAACCTTGAGACGATATATGAACCACTTCTAG 1068

RESULT 12

ABL40194
ID ABL40194 standard; cDNA; 1065 BP.
XX
XX ABL40194;
XX
XX 23-MAY-2002 (first entry)
XX
XX Human G protein-coupled receptor TGR17-4 encoding cDNA SEQ ID NO:11.
XX
XX Human; G protein-coupled receptor; TGR17-4; nootropic; antiinflammatory;
XX vasotropic; immunomodulator; cytostatic; gene therapy; protein therapy;
XX neurological; inflammatory; circulatory; degenerative; immune system;
XX digestive disease; cancer; gene; ss.
XX
XX Homo sapiens.
XX
XX
XX Key location/Qualifiers
XX CDS 1.1065
XX /tag= a
XX /partial
XX /product= "TGR17-4"
XX /note= "no stop codon given"
XX
XX MO200204640-A1.
XX
XX 17-JAN-2002.
XX
XX 06-JUL-2001; 2001WO-JP05878.
XX
XX 07-JUL-2000; 2000JP-0211989.
XX 18-DEC-2000; 2000JP-0383794.
XX
XX (TAKE) TAKEDA CHEM IND LTD.
XX
XX Moriya T, Ito T, Shintani Y, Miyajima N;
XX
XX WPI; 2002-179706/23.
XX P-PSDB; ABB06253.
XX
XX G-protein coupled receptor protein TGR17 of human origin and DNA
XX encoding it for diagnosis and treatment of cancer and circulatory and
XX other diseases associated with its expression -
XX
XX Claim 7; Page 125-126; 145pp; Japanese.
XX
XX The present invention describes a human guanine nucleotide binding
XX protein (G protein) coupled receptor protein designated TGR17, which has
XX 5 variant forms (TGR17-1 to TGR17-5) of the receptor protein having
XX additional residues at the N-terminal. The TGR17 proteins have nootropic,
XX antiinflammatory, vasotropic, immunomodulator and cytostatic activities.
XX The TGR17 polynucleotides and protein can be used in gene therapy and
XX protein therapy. G-protein coupled receptor proteins are cell membrane
XX molecules mediating the cellular response to a large variety of signalling
XX molecules. The TGR17 polynucleotides and proteins can be used in the
XX diagnosis, treatment and prevention of diseases including neurological,
XX inflammatory, circulatory, degenerative, immune system and digestive
XX diseases and cancer. The present sequence encodes human TGR17-4 from the
XX present invention.
XX
XX Sequence 1065 BP: 277 A; 214 C; 213 G; 361 T; 0 other;

Query Match 47.0%; Score 1065; DB 24; Length 1065;
Best Local Similarity 100.0%; Pred. No. 1.28-274;
Matches 1065; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1198 ATGCCCTTGACGAGCATTTCTTCATTGAGACCTTGGCTAACAAATATCTCTGAGA 1257
DB 1 ATGCCCTTGACGAGCATTTCTTCATTGAGACCTTGGCTAACAAATATCTCTGAGA 60

QY 1258 ATATTTGCTGGGTATAGCTTTCAATTAACCTGCTTGGAAATCTTTTGTCAATGCGATG 1317
DB 61 ATATTTGCTGGGTATAGCTTTCAATTAACCTGCTTGGAAATCTTTTGTCAATGCGATG 120

QY 1318 AGATCTTTCATTAAAGCTGAAAATACAACTACGCTATGTCATGAAATCTTTGTGT 1377
DB 121 AGATCTTTCATTAAAGCTGAAAATACAACTACGCTATGTCATGAAATCTTTGTGT 180

QY 1378 GCTGATTCGCTGATGAGGTGTCTTCTGTTGTTGGCAATTTTGGATATTAATACCGA 1437
DB 181 GCTGATTCGCTGATGAGGTGTCTTCTGTTGTTGGCAATTTTGGATATTAATACCGA 240

QY 1438 GGGCAGATCAGAAATATGCTGCTGCTGATGAGAGCGCTGACAGTCCGCTCATGGGG 1497
DB 241 GGGCAGATCAGAAATATGCTGCTGCTGATGAGAGCGCTGACAGTCCGCTCATGGGG 300

QY 1498 TTCTGCGCATGCTGTCACCGAAGTCTGTTCTGCTACTGACCTTGAATCTTGGAG 1557
DB 301 TTCTGCGCATGCTGTCACCGAAGTCTGTTCTGCTACTGACCTTGAATCTTGGAG 360

QY 1558 AAGTTCTGTCATGTCCTTCCCTTCAGTAACATTCGACCTGGAACCGACCTCA 1617
DB 361 AAGTTCTGTCATGTCCTTCCCTTCAGTAACATTCGACCTGGAACCGACCTCA 420

QY 1618 GTCACTCTCATTTGTCATCTGGAATGCGGGAATTTTAACTGTAATTCATTTGGAAAT 1677
DB 421 GTCACTCTCATTTGTCATCTGGAATGCGGGAATTTTAACTGTAATTCATTTGGAAAT 480

QY 1678 AAGATTAATTTTGGAAATCTTTTATGAGAAATGAGATGTTTCCCATTTATATGAC 1737
DB 481 AAGATTAATTTTGGAAATCTTTTATGAGAAATGAGATGTTTCCCATTTATATGAC 540

QY 1738 CAACAGAGATATGGAAGAAAGGATTTCTTGGAAATTTCTAGGTTGACCTG 1797
DB 541 CAACAGAGATATGGAAGAAAGGATTTCTTGGAAATTTCTAGGTTGACCTG 600

QY 1798 CTGCTTTTTCATCATATGTTTCTTCTATATTAATGTTCTGTTCCATTCAAAAACC 1857
DB 601 CTGCTTTTTCATCATATGTTTCTTCTATATTAATGTTCTGTTCCATTCAAAAACC 660

QY 1858 GCTTGCAGACACAGAAATGAGAAATGTTTGGAAAGAGTGGCTTTGCAATCGT 1917
DB 661 GCTTGCAGACACAGAAATGAGAAATGTTTGGAAAGAGTGGCTTTGCAATCGT 720

QY 1918 TTTCTTTTATAGTGTCTGATGCAATCTGCAATTCCTGATTTTGTATTAATC 1977
DB 721 TTTCTTTTATAGTGTCTGATGCAATCTGCAATTCCTGATTTTGTATTAATC 780

QY 1978 CTTTCCCTCTTCCGGTGAATATACAGACACATGACTTCTGATATGATTTTTC 2037
DB 781 CTTTCCCTCTTCCGGTGAATATATACAGACACATGACTTCTGATATGATTTTTC 840

QY 2038 CTTTCAATTAACATGCTTTGAAATCCATCTCTTATCTGCACACCACTTTTAAAG 2097
DB 841 CTTTCAATTAACATGCTTTGAAATCCATCTCTTATCTGCACACCACTTTTAAAG 900

QY 2098 GACAAGTTGAAACGCTGCGCACAAAATCATGAGAAATCAATTTCAAAATTAATAA 2157
DB 901 GACAAGTTGAAACGCTGCGCACAAAATCATGAGAAATCAATTTCAAAATTAATAA 960

QY 2158 AAAAGTTATATCATCATTTGTTGATGAGAGCTCTTCTCTGAAAATCTGGGTT 2217
DB 961 AAAAGTTATATCATCATTTGTTGATGAGAGCTCTTCTCTGAAAATCTGGGTT 1020

QY 2218 TTGAACAAATTAACCTTGAGACGATATATGAACCACTTCTC 2262
DB 1021 TTGAACAAATTAACCTTGAGACGATATATGAACCACTTCTC 1065

RESULT 13
ABZ42570
ID ABZ42570 standard; DNA; 2274 BP.
XX

AC AB242570;
XX 04-MAR-2003 (first entry)
XX Human G protein-coupled receptor LGR7 nucleotide seq ID NO:622.
DE
XX G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
XX growth-related disease; cell regeneration-related disease; AIDS; cancer;
XX immunological-related disease; osteoarthritis; allergy;
XX Alzheimer's disease; atherosclerosis; infection; osteoporosis; diabetes;
XX osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
XX graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
XX psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
XX mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
XX hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
XX ulcer; gene; ds.
XX Homo sapiens.
OS WO200261087-A2.
XX 08-AUG-2002.
XX 19-DEC-2001; 2001WO-US0107.
XX 19-DEC-2000; 2000US-257144P.
XX (LIFE-) LIFESPAN BIOSCIENCES INC.
XX Burner GC, Roush CL, Brown JP;
PI WPI; 2003-046718/04.
XX P-PSDB; ABP81724.
DR
XX New isolated antigenic peptides e.g., for G protein-coupled receptors
XX (GPCR), useful for diagnosing and designing drugs for treating
XX conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease,
XX cancer or autoimmune diseases -
XX
XX Disclosure; Fig 1; 523pp; English.
XX
XX The present invention describes antigenic peptides (I) comprising:
XX (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
XX acids. Also described: (1) an assay for the detection of a particular
XX G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
XX and (2) an isolated antibody having high specificity and high affinity
XX or avidity for a particular GPCR. (1) can be used as GPCR modulators and
XX in gene therapy. The antigenic peptides for GPCRs are useful in detecting
XX an antibody against a particular GPCR, and in the production of specific
XX antibodies. The peptides and antibodies are also useful for detecting the
XX presence or absence of corresponding GPCRs. The antigenic peptides for
XX GPCRs and antibodies are useful for diagnosing and designing drugs for
XX treating immune-related diseases, growth-related diseases, cell
XX regeneration-related disease, immunological-related cell proliferative
XX diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
XX atherosclerosis, bacterial, fungal, protozoan or viral infections,
XX osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
XX inflammation, allergies, Crohn's disease, diabetes, graft versus host
XX disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
XX anxiety, depression, schizophrenia, dementia, mental retardation, memory
XX loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension, memory
XX hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
XX any other disorder in which GPCRs are involved. The antibodies may be
XX used in immunosays and immunodiagnosis. AB242523 to AB242869 encode
XX GPCR proteins given in ABP81675 to ABP82018, which are used in the
XX exemplification of the present invention.
XX
XX Sequence 2274 BP; 669 A; 460 C; 421 G; 724 T; 0 other;
SO
Query Match 32.5%; Score 735; DB 25; Length 2274;
Best Local Similarity 60.9%; Pred. No. 3.9e-186;
Matches 1263; Conservative 0; Mismatches 785; Indels 27; Gaps 3;

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DB 148 GTGACGACTCGGGAAATCAGGCCGATGAGCAACTGTGAGACAAACAAATGATGTGCTC 207
QY 262 AACATATTTGACAGTGCATGGAATGCTAACA-----GCGTG 300
DB 208 ATGCAATTTGACAAATATTTTGCAGTACTACAAATATGATCTCCCATATCTTTTATAG 267
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QY 721 GTTAATTAATCTTAAGAGCTCTTCC---CAAGCAGATGTGTGCCAAATGCTCACTC 777
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QY 778 AACTGGGTGATTTGGAAGGCAATGAATTAAGTATCTCAAAATTTCAAGCTTCTGTCG 837
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QY 838 TGCATGCTGACAGTGTGTTTCTGCTAGAAATCAAAATGTTTGTCCAGAGAAG 897
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Db 2068 GAAATGATTCATCGGTTTGGTATTAATAAGACAAAGAAATCTATGAGCAAGAAAGT 2127
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Db 2128 CAGAAACATATGCTCCATTCATCTGGGTGA 2162

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RESULT 14
 AA25345
 ID AA25345 standard; cDNA; 2467 BP.
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AC AA25345;
XX 20-DEC-1999 (first entry)
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DE Human LGR7 long form nucleotide sequence.
XX
XX Human; LGR4; LGR5; LGR7; G-protein coupled receptor; gene therapy;
XX extracellular leucine rich repeat region; mapping; identification; ss.
XX
XX Homo sapiens.
XX
XX MO9948921-AI.
XX
XX 30-SEP-1999.
XX
XX 25-MAR-1999; 99WO-US06573.
XX
XX 26-MAR-1998; 98US-0079501.
XX
XX (STRD ) UNIV LELAND STANFORD JUNIOR.
XX
XX (ORCA ) ORGAMON NV.
XX
XX Hsueh AJW, Hsu SY, Liang S, Van Der Spek PJ;
XX
XX WPI; 1999-591074/50.
XX
XX P-PSDB; AAY42170.
XX
XX
XX New G-protein coupled receptors, useful for identifying their own
XX ligands -
XX
XX Claim 4; Fig 3; 54pp; English.
XX
XX
XX The present sequence encodes the human G-protein coupled receptor
XX having extracellular leucine rich repeat regions, designated LGR7 long
XX form. The LGR4, LGR5 and LGR7 proteins are used to identify ligands for
XX the receptor. The polypeptides and/or polynucleotides are also useful
XX for homologous or related genes, producing compositions that modulate
XX the expression or function of the receptors, gene therapy, mapping
XX functional regions of the receptors, studying associated physiological
XX pathways, in vivo prophylactic and therapeutic purposes, as immunogens
XX for producing antibodies, and for identifying biologically active
XX agents. The polypeptides contain a G-protein coupled seven
XX transmembrane region and a leucine rich repeat extracellular domain.
XX These regions capture and facilitate optimal orientation of its ligand.
XX The proteins are also expressed in diverse tissues.
XX
XX
XX Sequence 2467 BP; 747 A; 487 C; 474 G; 759 T; 0 other;
XX
XX
XX Query Match 32.5%; Score 735; DB 20; Length 2467;
XX Best Local Similarity 60.9%; Pred. No. 4.1e-186;
XX Matches 1263; Conservative 0; Mismatches 785; Indels 27; Gaps 3;
XX
Qy 142 GGAATTTTCCCTGGGGAATCTTACCAAGTCTTACCCGAGCTTTCACTGATGATGC 201
Db 281 GGCATTTTCCCTGGGGAATCTTACCAAGTCTTACCCGAGCTTTCACTGATGATGC 340
Qy 202 AAGATGATCTGGGGAACGGGCGGACGAAAGAACTGTGATGACATGATGATGCGG 261
Db 341 GTGACGATCTGGGGAACGGGCGGACGAAAGAACTGTGATGATGATGATGATGATG 400
Qy 262 ACCATATTTGGACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 300
Db 401 ATGCAATTTGGACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 460
Qy 301 GCTTAACACAGAGTCTTTCTTAAAGATATCCAAATGCTGATGATGATGATGATGATG 360
Db 461 GAGAAACACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 520
Qy 361 GAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
Db 521 GAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 580
Qy 421 TTACTGCTCTTAAGAAAAAACAATTCACAGTCTTCAAGATTAAGTTTCAATCAATAC 480

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PI Hsuen AJW, Hsu SY, Liang S, Van Der Spek PJ;
 XX WPI; 1999-591074/50.
 DR P-PSDB; AAY42171.
 XX
 PT New G-protein coupled receptors, useful for identifying their own
 PT ligands -
 XX
 PS Claim 4; Fig 4; 54pp; English.
 XX
 CC The present sequence encodes the human G-protein coupled receptor
 CC having extracellular leucine rich repeat regions, designated IGR7 short
 CC form. The IGRs, IGR5 and IGR7 proteins are used to identify ligands for
 CC the receptor. The polypeptides and/or polynucleotides are also useful
 CC for homologous or related genes, producing compositions that modulate
 CC the expression or function of the receptors, gene therapy, mapping
 CC functional regions of the receptors, studying associated physiological
 CC pathways, in vivo prophylactic and therapeutic purposes, as immunogens
 CC for producing antibodies, and for identifying biologically active
 CC agents. The polypeptides contain a G-protein coupled seven
 CC transmembrane region and a leucine rich repeat extracellular domain.
 CC These regions capture and facilitate optimal orientation of its ligand.
 CC The proteins are also expressed in diverse tissues.

XX Sequence 3584 BP; 1124 A; 670 C; 647 G; 1139 T; 4 other;

Query Match 30.3%; Score 686.2; DB 20; Length 3584;
 Best Local Similarity 62.0%; Pred. No. 5.7e-173;
 Matches 1122; Conservative 0; Mismatches 683; Indels 6; Gaps 2;

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 QY 505 CAGCATTAATGATTAAGACATATCCAGAAAGCATTTTGGATTATGTAATCTGAA 564
 DB 490 CAAAACATTAAGATTAACATCCATCCATCTATGCTTCAGAGACTGAATAGCTTACT 549
 QY 565 ATATTATATCTCAACCAACATGCTCAACCCCTCAGACCTGGAATTTCAAAACTTA 624
 DB 550 AACTGATCTCAGCATTAACAGAAATACCTTCGAAAGCGGGTGTGAAATCTT 609
 QY 625 CATCAGCTACTGCTAATTTCTAGATGACATCCAAATACAGAAATTTACAGGCTTG 684
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 DB 2050 CCAATCTCTATCTTCAACCAACTTTTAAAGCAAGTGAACAGCTCTGAT 2109

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GenCore version 5.1.6
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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4	2214	97.7	2214	11	US-09-965-536A-1
5	2111	93.2	2193	10	US-09-928-175-6
6	2060	90.9	2142	11	US-09-965-536A-5
7	1803	79.6	2049	10	US-09-928-175-11
8	1579.8	63.7	2539	14	US-10-223-735-4
9	1579	69.7	2214	10	US-09-928-175-19
10	1149	50.7	1149	10	US-09-928-175-4
11	1066.4	47.1	1068	12	US-10-321-807-17
12	995	43.9	1077	10	US-09-928-175-9
13	991	42.8	1101	10	US-09-928-175-16
14	825.8	36.5	1140	10	US-09-928-175-22
15	735	32.5	2274	14	US-10-223-567A-622
16	687	30.3	933	10	US-09-928-175-14

17	496.8	21.9	1804	10	US-09-895-686-10	Sequence 10, Appl
18	413	18.2	853	12	US-10-017-161-1325	Sequence 1325, Ap
19	370	16.3	592	9	US-09-811-284-43	Sequence 43, Appl
20	321	14.2	321	11	US-09-930-112-1	Sequence 1, Appl
21	265.4	11.8	760	10	US-09-764-877-1029	Sequence 1029, Ap
22	232.4	10.3	252	12	US-10-029-386-16266	Sequence 16266, A
23	232.4	10.3	571	12	US-10-029-386-2566	Sequence 2566, Ap
24	232.4	10.3	576	9	US-09-811-284-100	Sequence 100, App
25	227.6	10.0	1126	14	US-10-313-542-255	Sequence 255, App
26	227.6	9.8	612	10	US-09-895-686-37	Sequence 37, Appl
27	222	9.8	1018	11	US-09-782-874C-65	Sequence 65, Appl
28	221	9.8	562	10	US-09-895-686-38	Sequence 38, Appl
29	184.4	8.2	530	9	US-09-764-853-137	Sequence 137, App
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31	184.4	8.1	530	11	US-09-989-442-33	Sequence 33, Appl
32	184.4	8.1	530	12	US-09-764-886-18	Sequence 18, Appl
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34	184.4	8.1	530	14	US-10-103-313-89	Sequence 89, Appl
35	184.4	8.1	530	14	US-10-073-885-47	Sequence 47, Appl
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37	173	7.6	466	10	US-09-895-686-34	Sequence 34, Appl
38	173	7.6	719	12	US-09-814-353-18321	Sequence 18321, A
39	167.4	7.4	1228	12	US-10-353-690-19	Sequence 19, Appl
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41	150.4	6.6	677	12	US-09-814-353-11937	Sequence 11937, A
42	113.8	5.0	1080	14	US-10-270-333-26	Sequence 26, Appl
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44	81.2	3.6	1866	12	US-09-766-5118-22	Sequence 22, Appl
45	81.2	3.6	1866	12	US-10-188-495-47	Sequence 47, Appl

ALIGNMENTS

RESULT 1
US-09-928-175-1
Sequence 1, Application US/09928175
Patent No. US20020123618A1
GENERAL INFORMATION:
APPLICANT: Paszty, Christopher J.
APPLICANT: Gong, Jianhua
APPLICANT: Daugherty, Betsy
APPLICANT: Rogers, No. US20020123618A1a
TITLE OF INVENTION: Leucine-Rich G Protein Coupled Receptor-8 Molecules and
FILE REFERENCE: 00-1229
CURRENT APPLICATION NUMBER: US/09/928,175
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/224,455
PRIOR FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 1
LENGTH: 2265
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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NAME/KEY: sig_peptide
LOCATION: (1) .. (108)
US-09-928-175-1

Query Match 100.0%; Score 2265; DB 10; Length 2265;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2265; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGTTTTCGTTTAAACATCTTTCAGCTTCAGATTGATTAATGTTCTT 60
DB 1 ATGATGTTTTCGTTTAAACATCTTTCAGCTTCAGATTGATTAATGTTCTT 60
QY 61 CTACTGATTCATGCTGATCAATGTCAGATTTTGCACGATCAAGTATGATG 120
|||||

Db 61 CTACTTCATTCATCGTTCGATCAATGTCAAAGATTTTGGACGACGACGATGAGT 120
Qy 121 ATCACTCCTTCAAGCCAAAAGATATTTTCCCTGCGGAATCTTACCAAGCTTACC 180
Db 121 ATCACTCCTTCAAGCCAAAAGATATTTTCCCTGCGGAATCTTACCAAGCTTACC 180
Qy 181 CGAGCTTTCACTGATGAGCAAGATGACGTGCGGAGCGGGCGAGCAAGAACTGT 240
Db 181 CGAGCTTTCACTGATGAGCAAGATGACGTGCGGAGCGGGCGAGCAAGAACTGT 240
Qy 241 GGTGACACTAGATGAGTGGCGACCATATTTGGCAGCTGATGGAATGCTAACAGCGTG 300
Db 241 GGTGACACTAGATGAGTGGCGACCATATTTGGCAGCTGATGGAATGCTAACAGCGTG 300
Qy 301 GCGCTTAACACAGAGTCTTTCTTAAACAGTATCCAAATGCTGTGACGCAAGAACT 360
Db 301 GCGCTTAACACAGAGTCTTTCTTAAACAGTATCCAAATGCTGTGACGCAAGAACT 360
Qy 361 GAAATGGAAATGTAATGGTGAATTAAGTCTGCGGATGATTTCTTAACAATGTGCA 420
Db 361 GAAATGGAAATGTAATGGTGAATTAAGTCTGCGGATGATTTCTTAACAATGTGCA 420
Qy 421 TTAAGTCTCTTAAAGAAAACAAAATCCACAGTCTTCAGATAAAGTTTCACTCAATAC 480
Db 421 TTAAGTCTCTTAAAGAAAACAAAATCCACAGTCTTCAGATAAAGTTTCACTCAATAC 480
Qy 481 ACAAAACCTTAAAGAAATTTTCTTCAAGATTAATGCAATTTAGACAAATCCAGAAAGCA 540
Db 481 ACAAAACCTTAAAGAAATTTTCTTCAAGATTAATGCAATTTAGACAAATCCAGAAAGCA 540
Qy 541 TTTTGGATTAATGTAATCTGCAATATTTATATCTCAACCAACATGCAACACCTC 600
Db 541 TTTTGGATTAATGTAATCTGCAATATTTATATCTCAACCAACATGCAACACCTC 600
Qy 601 AGACCTGAATATTCAAAGACTTACATCAAGCTTAACTGGCTAATTTAGATGACATCA 660
Db 601 AGACCTGAATATTCAAAGACTTACATCAAGCTTAACTGGCTAATTTAGATGACATCA 660
Qy 661 ATAAACGAATTTCAAGCGCTGTTTAAACGGGATTTAAATTCCTGTTTCCCTGCTATG 720
Db 661 ATAAACGAATTTCAAGCGCTGTTTAAACGGGATTTAAATTCCTGTTTCCCTGCTATG 720
Qy 721 GTTATATACTACTAGAACTCTTCCCAAGCAGATGCTGCGCAAAATGCTCAACTCAAC 780
Db 721 GTTATATACTACTAGAACTCTTCCCAAGCAGATGCTGCGCAAAATGCTCAACTCAAC 780
Qy 781 TGGGTGATTTGGAAGCAATAGATAAATGATCTTCAAAATTTGACGTTCTGTGCTGC 840
Db 781 TGGGTGATTTGGAAGCAATAGATAAATGATCTTCAAAATTTGACGTTCTGTGCTGC 840
Qy 841 GATTCGCTCAAGTCTGTTCTGCTGATGAAATCAAAATTTGTTTCCAGAAAGCA 900
Db 841 GATTCGCTCAAGTCTGTTCTGCTGATGAAATCAAAATTTGTTTCCAGAAAGCA 900
Qy 901 TTTTCTTCAATTAATAATTTAGAGAACTGATCTGTCTAGCAATACGATTAACGAGTGA 960
Db 901 TTTTCTTCAATTAATAATTTAGAGAACTGATCTGTCTAGCAATACGATTAACGAGTGA 960
Qy 961 TCACCTCACTTTTAAAGACTTGAAGCTTCTTAAACAAAGCTGAACCTGTCTCAATCTT 1020
Db 961 TCACCTCACTTTTAAAGACTTGAAGCTTCTTAAACAAAGCTGTCTCAATCTT 1020
Qy 1021 CTTATGATCTTCAAGAAACCAAGTTGAAAGTCTTAAACAACTTCACTGATGAGCTG 1080
Db 1021 CTTATGATCTTCAAGAAACCAAGTTGAAAGTCTTAAACAACTTCACTGATGAGCTG 1080
Qy 1081 GAAAAGATAGAGATTCCAATATTAACAACAGATGTTTCAACCCATGAAGAACTTTCT 1140
Db 1081 GAAAAGATAGAGATTCCAATATTAACAACAGATGTTTCAACCCATGAAGAACTTTCT 1140
Qy 1141 CACATTTATTTCAAAAACCTTTCGATGATGCTCTATGCTCCCATGTCGAATATGATG 1200
Db 1141 CACATTTATTTCAAAAACCTTTCGATGATGCTCTATGCTCCCATGTCGAATATGATG 1200

Qy 1201 CCTTGAACGAGCGCAATTTCTTCAATTTAGAGACCTCTTGGCTTAAACAATATCCACAGAA 1260
Db 1201 CCTTGAACGAGCGCAATTTCTTCAATTTAGAGACCTCTTGGCTTAAACAATATCCACAGAA 1260
Qy 1261 TTTGTCTGGGTTATAGCTTTCATTAACCTGCTTGGAAATCTTTTGTCTATGGCATGAG 1320
Db 1261 TTTGTCTGGGTTATAGCTTTCATTAACCTGCTTGGAAATCTTTTGTCTATGGCATGAG 1320
Qy 1321 TCTTTCATTAAGCTGAAATATCACTCAAGCTATGCTCAATCAAAATCTTTGTGTCT 1380
Db 1321 TCTTTCATTAAGCTGAAATATCACTCAAGCTATGCTCAATCAAAATCTTTGTGTCT 1380
Qy 1381 GATTCGCTGATGGGTTTATCTTGTCTTGTGGATTTTGAATTAATAATACAGAGG 1440
Db 1381 GATTCGCTGATGGGTTTATCTTGTCTTGTGGATTTTGAATTAATAATACAGAGG 1440
Qy 1441 CAGTATCAGAAAGTATCCTTGTGCTGATGAGAGAGCTGCAAGTCCGCTCATGGGTTTC 1500
Db 1441 CAGTATCAGAAAGTATCCTTGTGCTGATGAGAGAGCTGCAAGTCCGCTCATGGGTTTC 1500
Qy 1501 CTGGCAATGCTGTCCACCGAAGCTCTGTCTGCTACTGACCTTGAATTTGGAGAG 1560
Db 1501 CTGGCAATGCTGTCCACCGAAGCTCTGTCTGCTACTGACCTTGAATTTGGAGAG 1560
Qy 1561 TTTCTGATCATGCTTCCCTTCACTTAACTTCACTGATGAGAGAGAGAGAGAGAGAG 1620
Db 1561 TTTCTGATCATGCTTCCCTTCACTTAACTTCACTGATGAGAGAGAGAGAGAGAGAGAG 1620
Qy 1621 ATCCATATTTGCACTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1680
Db 1621 ATCCATATTTGCACTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1680
Qy 1681 GATTTATTTGGAACCTTTATAGGGAATAATAGAGATGTTTCCCATTTATATGACCA 1740
Db 1681 GATTTATTTGGAACCTTTATAGGGAATAATAGAGATGTTTCCCATTTATATGACCA 1740
Qy 1741 ACAGAAAGATTTGGAAGCAAAAGGATTTCTTGGAAATTTTCTTGAAGTGAATCTGCT 1800
Db 1741 ACAGAAAGATTTGGAAGCAAAAGGATTTCTTGGAAATTTTCTTGAAGTGAATCTGCT 1800
Qy 1801 GCTTTCTCATCATGTTGTTTCTTATATTAATGATGTTCTTCAATCAAAACCGCC 1860
Db 1801 GCTTTCTCATCATGTTGTTTCTTATATTAATGATGTTCTTCAATCAAAACCGCC 1860
Qy 1861 TTGCAAGCCACAGAGTGAAGAAATGTTTGGAAAGAGAGAGAGAGAGAGAGAGAGAG 1920
Db 1861 TTGCAAGCCACAGAGTGAAGAAATGTTTGGAAAGAGAGAGAGAGAGAGAGAGAGAG 1920
Qy 1921 TTTTATATGATGTTCTGATGCAATCTGCTGATCTGATATTTGATTAATAATCTT 1980
Db 1921 TTTTATATGATGTTCTGATGCAATCTGCTGATCTGATATTTGATTAATAATCTT 1980
Qy 1981 TCCCTCTTCCGGGTGGAATATCAAGACCAATGATCTTCTGATATGATTTTCTTCT 2040
Db 1981 TCCCTCTTCCGGGTGGAATATCAAGACCAATGATCTTCTGATATGATTTTCTTCT 2040
Qy 2041 CCAAGTTAAGAGTGTGATTCGAATCTCTATATCTGCAACAACCACTTTTAAAGAC 2100
Db 2041 CCAAGTTAAGAGTGTGATTCGAATCTCTATATCTGCAACAACCACTTTTAAAGAC 2100
Qy 2101 AAGTTGAACAGCTGCTGCAAAACATCAGAGGAATCAATTTTCAAAATTAATAAAAA 2160
Db 2101 AAGTTGAACAGCTGCTGCAAAACATCAGAGGAATCAATTTTCAAAATTAATAAAAA 2160
Qy 2161 AGTTTATCTATTCATCTGTTGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2220
Db 2161 AGTTTATCTATTCATCTGTTGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2220
Qy 2221 AACAAATTAACAATTTGAGAGAGAGATTAATGAACCAAGTTTCTAG 2265
Db 2221 AACAAATTAACAATTTGAGAGAGAGATTAATGAACCAAGTTTCTAG 2265

```
RESULT 2
US-10-222-668-1
; Sequence 1, Application US/10222668
; Publication No. US2003088884A1
; GENERAL INFORMATION:
; APPLICANT: Heueh, Aaron
; TITLE OF INVENTION: Mammalian Relaxin Receptor
; FILE REFERENCE: STAN-239 MO
; CURRENT APPLICATION NUMBER: US/10/222,668
; PRIORITY FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/313,259
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 1
; LENGTH: 2838
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (107)...(2369)
US-10-222-668-1

Query Match      100.0%; Score 2265; DB 14; Length 2838;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2265; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGATGTTTTTCTGCTTTTAAACATCTCTTACGCTTCAAGTATGATTAACAATGTTCTT 60
DB 107 ATGATGTTTTTCTGCTTTTAAACATCTCTTACGCTTCAAGTATGATTAACAATGTTCTT 166
QY 61 CTACTCATTTTCATGCTCTGATGCAATGCAAGATTTTGCACTGACCTCAAGTATGCAATG 120
DB 167 CTACTCATTTTCATGCTCTGATGCAATGCAAGATTTTGCACTGACCTCAAGTATGCAATG 226
QY 121 ATCACTCTCTTCAATGCAAGATTAATTTTCCCTGCGGAATCTTACCAAGTCTTACCC 180
DB 227 ATCACTCTCTTCAATGCAAGATTAATTTTCCCTGCGGAATCTTACCAAGTCTTACCC 286
QY 181 CGAGCTTTTCACTGATGAGCAAGATGACTGTGGGAACGGGGCGGAGCAAGAGAACTGT 240
DB 287 CGAGCTTTTCACTGATGAGCAAGATGACTGTGGGAACGGGGCGGAGCAAGAGAACTGT 346
QY 241 GGTGACACTAGTGAATGGGCGACCATATTTGGCAGAGTGCATGGAATGCTAACAGCGTG 300
DB 347 GGTGACACTAGTGAATGGGCGACCATATTTGGCAGAGTGCATGGAATGCTAACAGCGTG 406
QY 301 GCCTTAACACAGAGTGTCTTTCTAAACAGATTCACAAATGCTGTGACCTGCAAGAAACT 360
DB 407 GCCTTAACACAGAGTGTCTTTCTAAACAGATTCACAAATGCTGTGACCTGCAAGAAACT 466
QY 361 GAATGGAATGTGTAATGTGATTAAGTCTGTGCGCATATTTCTTAACAATGTGACA 420
DB 467 GAATGGAATGTGTAATGTGATTAAGTCTGTGCGCATATTTCTTAACAATGTGACA 526
QY 421 TTACTGTCTTAAAGAAAACAAATCCACAGTCTTCCAGATTAAGTTTCTATCAATATAC 480
DB 527 TTACTGTCTTAAAGAAAACAAATCCACAGTCTTCCAGATTAAGTTTCTATCAATATAC 586
QY 481 ACAAACCTTAAGAAATATTTCTTACAGATTAATGATTAAGACATATCCAGAAAGCA 540
DB 587 ACAAACCTTAAGAAATATTTCTTACAGATTAATGATTAAGACATATCCAGAAAGCA 646
QY 541 TTTTGTGATTAATGTAATGTAATATTAATATTCACACACACAGTGTCAACACCTTC 600
DB 647 TTTTGTGATTAATGTAATGTAATATTAATATTCACACACACAGTGTCAACACCTTC 706
QY 601 AGACCTGGAATATTCACAAAGCTTACATCAGTAACTTGGCTAATTTAGATGACATCA 660
DB 707 AGACCTGGAATATTCACAAAGCTTACATCAGTAACTTGGCTAATTTAGATGACATCA 766
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QY 661 ATAAACAGAAATTTTCAACAGCGCTTTTACGGGATTAATTCCTGTTTTCTGTCTATG 720
DB 767 ATAAACAGAAATTTTCAACAGCGCTTTTACGGGATTAATTCCTGTTTTCTGTCTATG 826
QY 721 GTTAATACTAATTAGAGCTCTTCCCAAGAGATGTGCGCAATGCTCAACTCAAC 780
DB 827 GTTAATACTAATTAGAGCTCTTCCCAAGAGATGTGCGCAATGCTCAACTCAAC 886
QY 781 TGGGTGATTTGGAAGCAATAGAAATTAAGATCTCAAAATTCAGTTTCTGTGCGC 840
DB 887 TGGGTGATTTGGAAGCAATAGAAATTAAGATCTCAAAATTCAGTTTCTGTGCGC 946
QY 841 GATTGCTCAACAGTGTCTTCTGCTTCAAGATTAATGATTTGTTTCCAGAGAGCA 900
DB 947 GATTGCTCAACAGTGTCTTCTGCTTCAAGATTAATGATTTGTTTCCAGAGAGCA 1006
QY 901 TTTTCTTCAATTAATAATTTTGAAGAACTGATCTGTCTAGCATATGATTAAGAGCTA 960
DB 1007 TTTTCTTCAATTAATAATTTTGAAGAACTGATCTGTCTAGCATATGATTAAGAGCTA 1066
QY 961 TCACCTCAACCTTTTAAAGACTTGAAGCTTCAACAAAGCTGAACCTGATCCATCT 1020
DB 1067 TCACCTCAACCTTTTAAAGACTTGAAGCTTCAACAAAGCTGATCCATCT 1126
QY 1021 CTATATGATCTTCAACAAAGCAAGTTGAAGTCTTAAACAATCTCACTCTAGACCTG 1080
DB 1127 CTATATGATCTTCAACAAAGCAAGTTGAAGTCTTAAACAATCTCACTCTAGACCTG 1186
QY 1081 GAAAGATAGAGATTTCCAAATATTAACAACAGAAATGTTTCAACCCATGAAGAACTTTCT 1140
DB 1187 GAAAGATAGAGATTTCCAAATATTAACAACAGAAATGTTTCAACCCATGAAGAACTTTCT 1246
QY 1141 CAGATTTATTTCAAAAACCTTTCAGATACGCTCTGATGCTCCAGTCCGAATATGATG 1200
DB 1247 CAGATTTATTTCAAAAACCTTTCAGATACGCTCTGATGCTCCAGTCCGAATATGATG 1306
QY 1201 CCTTGAAGAGCGGCAATTTCTTCAATTTGAAGGACCTTTGAGTAAACAATATCTCAGAAAT 1260
DB 1307 CCTTGAAGAGCGGCAATTTCTTCAATTTGAAGGACCTTTGAGTAAACAATATCTCAGAAAT 1366
QY 1261 TTTGTCTGGGTAAATAGCTTTTCAATTAACCTGCTTTGGAATCTTTTGTGATGGAATGGA 1320
DB 1367 TTTGTCTGGGTAAATAGCTTTTCAATTAACCTGCTTTGGAATCTTTTGTGATGGAATGGA 1426
QY 1321 TCTTTCATTAAGCTGAAGAAATATCAACTCAACCTATGTCATCAAAATCTTTGTGTGCT 1380
DB 1427 TCTTTCATTAAGCTGAAGAAATATCAACTCAACCTATGTCATCAAAATCTTTGTGTGCT 1486
QY 1381 GATTGCTGATGGGTGTTTACTGTCTTTGTGGCATTTTGCATTAATAAATATCCAGAGG 1440
DB 1487 GATTGCTGATGGGTGTTTACTGTCTTTGTGGCATTTTGCATTAATAAATATCCAGAGG 1546
QY 1441 CAGATTCAGAGATATGCTTCTGTGATGAATGAAGCGGCGAGTCCGCTCATAGGGGTTC 1500
DB 1547 CAGATTCAGAGATATGCTTCTGTGATGAATGAAGCGGCGAGTCCGCTCATAGGGGTTC 1606
QY 1501 CTGGCATGCTGTCCACCGAAGTCTCTGTCTGCTACTGACCTTACTGATCTTTGAGAGAG 1560
DB 1607 CTGGCATGCTGTCCACCGAAGTCTCTGTCTGCTACTGACCTTACTGATCTTTGAGAGAG 1666
QY 1561 TTCTGTGATATTTCTTCCCTTCAATGATTAATGCACTGGAAGGCGAGACCTCACTC 1620
DB 1667 TTCTGTGATATTTCTTCCCTTCAATGATTAATGCACTGGAAGGCGAGACCTCACTC 1726
QY 1621 ATCCCTATTTGATGATGATGAGCGGAGTTTATATGATGATTAATGCACTTTTGAATAG 1680
DB 1727 ATCCCTATTTGATGATGATGAGCGGAGTTTATATGATGATTAATGCACTTTTGAATAG 1786
QY 1681 GATTATTTTGGAAACTTTTATGAGGAAATATGAGATGTTTCCCACTTATATATGACCA 1740
DB 1787 GATTATTTTGGAAACTTTTATGAGGAAATATGAGATGTTTCCCACTTATATATGACCA 1846
QY 1741 ACAAGAGATATTTGAAGCAAGGATTTCTCTTGAATTTTCTTGAATGATGATCTTGGC 1800
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Db 1847 ACGAAGATATTGGAAGCAAGGATATTCCTTGGATTTTCTAGGTGGAACCTTGCG 1906
Qy 1801 GCTTTTCTCATCTGTGTGTTTCCCTATATTACTATGTTCTGTTCCATTCAAAAACCCGC 1860
Db 1907 GCTTTTCTCATCTGTGTGTTTCCCTATATTACTATGTTCTGTTCCATTCAAAAACCCGC 1966
Qy 1861 TTGACAGCCACAGAGTAAGGAATGTTTGGAGAGAGGTGGCTGTGCAAAATCGTTC 1920
Db 1967 TTGACAGCCACAGAGTAAGGAATGTTTGGAGAGAGGTGGCTGTGCAAAATCGTTC 2026
Qy 1921 TTTTATATAGTGTCTCTGATGCAATCTGCTGATTCCTGTATTTGATTAATTCCT 1980
Db 2027 TTTTATATAGTGTCTCTGATGCAATCTGCTGATTCCTGTATTTGATTAATTCCT 2086
Qy 1981 TCCCTCTTCCGGGTGGAATATACAGACACATGACTTCTGTAGTATGATTTTTCCT 2040
Db 2087 TCCCTCTTCCGGGTGGAATATACAGACACATGACTTCTGTAGTATGATTTTTCCT 2146
Qy 2041 CCAGTTAAGAGTCTTGAATCCATCTATCTGACAACTTTTAAAGAC 2100
Db 2147 CCAGTTAAGAGTCTTGAATCCATCTATCTGACAACTTTTAAAGAC 2206
Qy 2101 AAGTTGAAACAGCTGTGCAAAACATCAGAGGAATCAATTTTCAAAATTAATAAAAA 2160
Db 2207 AAGTTGAAACAGCTGTGCAAAACATCAGAGGAATCAATTTTCAAAATTAATAAAAA 2266
Qy 2161 AGTTTATCTACATCCATGTTGTGATGATGAGACCTCTCTCCCTGAAACCTTGGGCTTC 2220
Db 2267 AGTTTATCTACATCCATGTTGTGATGATGAGACCTCTCTCCCTGAAACCTTGGGCTTC 2326
Qy 2221 AACAAATAACACTTGAGAGACAGTATATGAAACCAAGTTTCTAG 2265
Db 2327 AACAAATAACACTTGAGAGACAGTATATGAAACCAAGTTTCTAG 2371

RESULT 3
US-10-229-735-2
; Sequence 2, Application US/10229735
; Publication No. US20030082650A1
; GENERAL INFORMATION:
; APPLICANT: Baylor College of Medicine
; APPLICANT: Agoulnik, Alexander I.
; TITLE OF INVENTION: The GREAT Gene and Protein
; FILE REFERENCE: 7572/73263
; CURRENT APPLICATION NUMBER: US/10/229, 735
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 60/315, 696
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 60/351, 432
; PRIOR FILING DATE: 2002-01-28
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 2436
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-229-735-2

Query Match 99.9%; Score 2261.8; DB 14; Length 2436;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2263; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGATGTTTTTCTGTTTTTAAACATCTCTTACGCTCAGATTGATTACAAATGTTCTT 60
Db 71 ATGATGTTTTTCTGTTTTTAAACATCTCTTACGCTCAGATTGATTACAAATGTTCTT 130
Qy 61 CTACTTCATTTTCATCGTTCTGATCAATGTCAAGATTTTGCAGTCAAGAGTAGATG 120
Db 131 CTACTTCATTTTCATCGTTCTGATCAATGTCAAGATTTTGCAGTCAAGAGTAGATG 190
Qy 121 ATCCTCTTATGCGCAAAAGATATTTTCCCTGTGGATCTTACCAATGCTTACCC 180

Db 191 ATCACTCTTCAAGCCAAAAGATATTTTCCCTGTGGATCTTACCAATGCTTACCC 250
Qy 181 CGAGCTTTTCACTGATGATGCAAGATGATCTGTGGAAACGGGGCGGACGAGAGATCTG 240
Db 251 CGAGCTTTTCACTGATGATGCAAGATGATCTGTGGAAACGGGGCGGACGAGAGATCTG 310
Qy 241 GGTGACATGATGATGAGCGACATATTTGGACAGTGCATGAAATGCTAACAGCTG 300
Db 311 GGTGACATGATGATGAGCGACATATTTGGACAGTGCATGAAATGCTAACAGCTG 370
Qy 301 GCTTAAACACAGAGTCTTTCTTAAACATGATCCACATGCTGTGACCTGCAAAAGT 360
Db 371 GCTTAAACACAGAGTCTTTCTTAAACATGATCCACATGCTGTGACCTGCAAAAGT 430
Qy 361 GAATGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
Db 431 GAATGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 490
Qy 421 TTAAGTCTCTTAAAGAAAACAAAATCCACAGTCTTCCAGATTAAGTTTCAATAC 480
Db 491 TTAAGTCTCTTAAAGAAAACAAAATCCACAGTCTTCCAGATTAAGTTTCAATAC 550
Qy 481 ACAAACCTTAAAGATATTTCTTCAAGATTAATGATTAACATATCCAGAAAGCA 540
Db 551 ACAAACCTTAAAGATATTTCTTCAAGATTAATGATTAACATATCCAGAAAGCA 610
Qy 541 TTTTGTGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATG 600
Db 611 TTTTGTGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATGATTAATG 670
Qy 601 AAGCTGGAATATTCAGAGGCTTGTGATGAGGATTAATTCCTGTTTTCGTCTATG 720
Db 671 AAGCTGGAATATTCAGAGGCTTGTGATGAGGATTAATTCCTGTTTTCGTCTATG 790
Qy 721 GTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 780
Db 791 GTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 850
Qy 781 TGGGTGATTTGGAAGCAATGATTAATTAATTAATTAATTAATTAATTAATTAATTA 840
Db 851 TGGGTGATTTGGAAGCAATGATTAATTAATTAATTAATTAATTAATTAATTAATTA 910
Qy 841 GATTCCTCAACAGTCTGTTTCTGCTTAAGAAATCAATGTTTGTCCAGAGAGACA 900
Db 911 GATTCCTCAACAGTCTGTTTCTGCTTAAGAAATCAATGTTTGTCCAGAGAGACA 970
Qy 901 TTTTCTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 960
Db 971 TTTTCTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1030
Qy 961 TCACTCACTTTTAAAGCTTGAAGCTTCAAAAGCTGAACCTGTCAATCAATCTT 1020
Db 1031 TCACTCACTTTTAAAGCTTGAAGCTTCAAAAGCTGAACCTGTCAATCAATCTT 1090
Qy 1021 CTATGATCTTCAAGAAACAGTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTT 1080
Db 1091 CTATGATCTTCAAGAAACAGTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTT 1150
Qy 1081 GAAAGATGAGATTCATTAATTAACACAGATGTTTCAACCCATGAAGATCTTCT 1140
Db 1151 GAAAGATGAGATTCATTAATTAACACAGATGTTTCAACCCATGAAGATCTTCT 1210
Qy 1141 CACATTTATTTCAAAAACCTTGAATCTGTCTTAAGTCCCAATGCGAATATGATG 1200
Db 1211 CACATTTATTTCAAAAACCTTGAATCTGTCTTAAGTCCCAATGCGAATATGATG 1270
Qy 1201 CCGTGAACGAGCAATTTCTTCAATTTGAGACCTCTTGGCTTAACATATCTCAGATA 1260
Db 1271 CCGTGAACGAGCAATTTCTTCAATTTGAGACCTCTTGGCTTAACATATCTCAGATA 1330

1261 TTGTCGGGTTAGTTCATTAACGCTTGGAAATCTTTTGCATTTGGATGAGA 1320
1331 TTGTCGGGTTAGTTCATTAACGCTTGGAAATCTTTTGCATTTGGATGAGA 1390
1321 TCCTTCAATTAAGCTGAATAATACACCTGATGTCATCAAAATCTTTGTTGCT 1380
1391 TCCTTCAATTAAGCTGAATAATACACCTGATGTCATCAAAATCTTTGTTGCT 1450
1381 GATTGCTGATGGGTGTTTACTTGTCTTTGTTGGCATTTTGCATTAATAATACGAGGG 1440
1451 GATTGCTGATGGGTGTTTACTTGTCTTTGTTGGCATTTTGCATTAATAATACGAGGG 1510
1441 CAGTATGAGAGTATGCTGCTGATGAGAGCGGAGTGGCGGCTCATGGGGTTC 1500
1511 CAGTATGAGAGTATGCTGCTGATGAGAGCGGAGTGGCGGCTCATGGGGTTC 1570
1501 CTGGCCATGCTGTCCACCGAAGTCTGTCTGCTACTGACCTTACTTTGGAGAG 1560
1571 CTGGCCATGCTGTCCACCGAAGTCTGTCTGCTACTGACCTTACTTTGGAGAG 1630
1561 TTCTGCTGATGCTTCTCCCTTCACTAATGATGAGCTGAGAAAACGCAAGCTCAGTC 1620
1631 TTCTGCTGATGCTTCTCCCTTCACTAATGATGAGCTGAGAAAACGCAAGCTCAGTC 1690
1621 ATCCCTCATTTGCTGATGAGAGCGGATTTTAAATAGCTGTAATTCATTTGGAAATAG 1680
1691 ATCCCTCATTTGCTGATGAGAGCGGATTTTAAATAGCTGTAATTCATTTGGAAATAG 1750
1681 GATTATTTTGGAAATCTTTTATGAGAAATGAGATGTTTCCCATTTATATGACCAA 1740
1751 GATTATTTTGGAAATCTTTTATGAGAAATGAGATGTTTCCCATTTATATGACCAA 1810
1741 ACAGAAATATTTGAGAAAGGATTTCTTGGAAATTTCTGATGCTGATGCTGCTG 1800
1811 ACAGAAATATTTGAGAAAGGATTTCTTGGAAATTTCTGATGCTGATGCTGCTG 1870
1801 GCTTTTCTCATCATTTGTTTCTTCTAATATGATGCTGCTGCTGCTGCTGCTGCTG 1860
1871 GCTTTTCTCATCATTTGTTTCTTCTAATATGATGCTGCTGCTGCTGCTGCTGCTG 1930
1861 TTGACAGCAACAGATGAGAAATGTTTGGAGAGAGTGGCTGTTGCAATGCTTTC 1920
1931 TTGACAGCAACAGATGAGAAATGTTTGGAGAGAGTGGCTGTTGCAATGCTTTC 1990
1921 TTTTATAGTGTCTGATGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1980
1991 TTTTATAGTGTCTGATGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2050
1981 TCCCTCTTCCGGGTGGAATACAGACAAATGATGCTGCTGCTGCTGCTGCTGCTG 2040
2051 TCCCTCTTCCGGGTGGAATACAGACAAATGATGCTGCTGCTGCTGCTGCTGCTG 2110
2041 CCAAGTTAAGTGTGTTGAATTCCTTCTAATGCTGCTGCTGCTGCTGCTGCTGCTG 2100
2111 CCAAGTTAAGTGTGTTGAATTCCTTCTAATGCTGCTGCTGCTGCTGCTGCTGCTG 2170
2101 AAGTTGAACAGCTGCTGCAAAATCATGAGGAAATCAATTTTCAAAATTAATAA 2160
2171 AAGTTGAACAGCTGCTGCAAAATCATGAGGAAATCAATTTTCAAAATTAATAA 2230
2161 AGTTATATGATGCTGCTGATGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2220
2231 AGTTATATGATGCTGCTGATGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2290
2221 AACAAATATGACCTTGGAGACAGTATTAATGAACCAAGTTTCTAG 2265
2291 AACAAATATGACCTTGGAGACAGTATTAATGAACCAAGTTTCTAG 2335

RESULT 4
US-09-965-536A-1
; Sequence 1, Application US/09965536A

Publication No. US20030027323A1
; GENERAL INFORMATION:
; APPLICANT: FEDER, J. N.
; APPLICANT: WINTER, G.
; APPLICANT: RAMANATHAN, C. S.
; APPLICANT: HAKKEN, D. R.
; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGBRBNYS,
; TITLE OF INVENTION: EXPRESSED HIGHLY IN BRAIN AND OVARIAN TISSUES
; FILE REFERENCE: D0041NP
; CURRENT APPLICATION NUMBER: US/09/965,536A
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/235,713
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/261,781
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 60/306,605
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/310,436
; PRIOR FILING DATE: 2001-08-03
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2214
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-965-536A-1
Query Match 97.7%; Score 2214; DB 11; Length 2214;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2214; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; 52 ATGTTCTTTCTACTTCAATTCATGCTGCTGATGCAATGCTCAAAAGATTTGGACTGACCTCAA 111
; 1 ATGTTCTTTCTACTTCAATTCATGCTGCTGATGCAATGCTCAAAAGATTTGGACTGACCTCAA 60
; 112 GTGATGATGATCACTCTTCAATGCGCAAAAGATATTTTCCCTGGGAAATCTTACCAAG 171
; 61 GTGATGATGATCACTCTTCAATGCGCAAAAGATATTTTCCCTGGGAAATCTTACCAAG 120
; 172 TGCTTACCCCGAGCTTTTCACTGATGAGCAAGATGATGCTGGGAAACGGGGCGGAGCAA 231
; 121 TGCTTACCCCGAGCTTTTCACTGATGAGCAAGATGATGCTGGGAAACGGGGCGGAGCAA 180
; 232 GAGAAGCTGTGTGATCACTAGTGTGAGGAGCAATATTTGGACAGTGTGCAATGAAATGCT 291
; 181 GAGAAGCTGTGTGATCACTAGTGTGAGGAGCAATATTTGGACAGTGTGCAATGAAATGCT 240
; 292 AACAGCTGTGCTTACACAGAGAGTCTTTCTAATAACAGTATCCAAATGCTGTGACTGC 351
; 241 AACAGCTGTGCTTACACAGAGAGTCTTTCTAATAACAGTATCCAAATGCTGTGACTGC 300
; 352 AAAAAGCTGAATGGAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATG 411
; 301 AAAAAGCTGAATGGAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATG 360
; 412 AATGTGACATTAAGTGTCTTAAAGAAACAAATTCACAGTCTTCCAGATTAAGATTTTC 471
; 361 AATGTGACATTAAGTGTCTTAAAGAAACAAATTCACAGTCTTCCAGATTAAGATTTTC 420
; 472 ATCAATATACCAAAATTTAAAGATATTTCTTCAAGATTAATGCAATGCAATGCAATG 531
; 421 ATCAATATACCAAAATTTAAAGATATTTCTTCAAGATTAATGCAATGCAATGCAATG 480
; 532 AGGAAACATTTTGGATTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTA 591
; 481 AGGAAACATTTTGGATTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTA 540
; 592 ACAACCTCAGACCTGGAATATTCAAAGACCTTACATGAGTAACTTGGCTAATTTCTAGAT 651
; 541 ACAACCTCAGACCTGGAATATTCAAAGACCTTACATGAGTAACTTGGCTAATTTCTAGAT 600
; 652 GACAATCAATTAACAGAAATTTTACAGCGCTTGTGTTACGGGATTAATTCCTGTTTTC 711

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 Db 661 CTGCTATGTTAATPACTACTTAAAGCTTTCCCAAGCAGATGTGSCCAATGCTT 720
 Qy 772 CAACCAATCTGGGTGGATTTGGAAGGCAATAGAAATTAAGTATCTCAAAATCTACGTTT 831
 Db 721 CAACCAATCTGGGTGGATTTGGAAGGCAATAGAAATTAAGTATCTCAAAATCTACGTTT 780
 Qy 832 CTGCTGTCGATTCGCTCAAGTGTGTTCTGCTTGAAGATCAATGCTTTGTTTCCA 891
 Db 781 CTGCTGTCGATTCGCTCAAGTGTGTTCTGCTTGAAGATCAATGCTTTGTTTCCA 840
 Qy 892 GAGAGACATTTTCTTCAATTAATAAATTTAGAGAACTGATCTGCTTGCATATAGATA 951
 Db 841 GAGAGACATTTTCTTCAATTAATAAATTTAGAGAACTGATCTGCTTGCATATAGATA 900
 Qy 952 AGGAGCTATCACTCACTTTTAAAGCTTGAAGCTTCAAAAGCTGAACCTGTCA 1011
 Db 901 AGGAGCTATCACTCACTTTTAAAGCTTGAAGCTTCAAAAGCTGAACCTGTCA 960
 Qy 1012 TCCATCTCTTATGATCTTCAAGAAACAGTTTGAAGCTTAAAGCACTTCACTGT 1071
 Db 961 TCCATCTCTTATGATCTTCAAGAAACAGTTTGAAGCTTAAAGCACTTCACTGT 1020
 Qy 1072 CTAGACTGGAAAGATAGAGATTCAAATATTAACACAGATGTTTCAACCCATGAAG 1131
 Db 1021 CTAGACTGGAAAGATAGAGATTCAAATATTAACACAGATGTTTCAACCCATGAAG 1080
 Qy 1132 AATCTTCTCAATTTATTTCAAAAATTGATGATGCTCTATGCTCCCATGTCGA 1191
 Db 1081 AATCTTCTCAATTTATTTCAAAAATTGATGATGCTCTATGCTCCCATGTCGA 1140
 Qy 1192 ATATGATGCTCTTGAAGGAGCTTCTCAATTTGAGAGCTTGTGCTAACAATATC 1251
 Db 1141 ATATGATGCTCTTGAAGGAGCTTCTCAATTTGAGAGCTTGTGCTAACAATATC 1200
 Qy 1252 CTGAGAAATTTTGTGCTGTTAATAGCTTATACCTGCTTGAAGCTTTTGTGCTAT 1311
 Db 1201 CTGAGAAATTTTGTGCTGTTAATAGCTTATACCTGCTTGAAGCTTTTGTGCTAT 1260
 Qy 1312 GGCATGAGATCTTCAATTAAGCTGAATAATACCACTGACCTATGTCATCAAAATCTT 1371
 Db 1261 GGCATGAGATCTTCAATTAAGCTGAATAATACCACTGACCTATGTCATCAAAATCTT 1320
 Qy 1372 TGTGTCGATGATGCTGATGAGGTGTTACTGTTCTTGTGCTGATTTTGCATATATAA 1431
 Db 1321 TGTGTCGATGATGCTGATGAGGTGTTACTGTTCTTGTGCTGATTTTGCATATATAA 1380
 Qy 1432 TACCGAGGAGATATGAGATATGCTTGTGCTGATGAGAGGCTGATGCTGCTC 1491
 Db 1381 TACCGAGGAGATATGAGATATGCTTGTGCTGATGAGAGGCTGATGCTGCTC 1440
 Qy 1492 ATGAGGATCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1551
 Db 1441 ATGAGGATCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
 Qy 1552 TTGAGGAAGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1611
 Db 1501 TTGAGGAAGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560
 Qy 1612 ACCCTGATCATCTCATTTTGTGATGATGAGGAGGATTTTAAATAGCTGATATTCATTT 1671
 Db 1561 ACCCTGATCATCTCATTTTGTGATGATGAGGAGGATTTTAAATAGCTGATATTCATTT 1620
 Qy 1672 TGAATTAAGATTAATTTTGAAGCTTTTATGAGAAAAATGAGATATGTTTCCACTTAT 1731
 Db 1621 TGAATTAAGATTAATTTTGAAGCTTTTATGAGAAAAATGAGATATGTTTCCACTTAT 1680
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 Db 1681 TATATCAAAAGAGATATTTGAGAGCAAGGATATCTCTTGAATTTTCTTATGATGCTG 1740

Qy 1792 AACTTGTGCTTTTCTCATGATGTTGTTTCTATATTAATAGTGTGTTCCATGCA 1851
 Db 1741 AACTTGTGCTTTTCTCATGATGTTGTTTCTATATTAATAGTGTGTTCCATGCA 1800
 Qy 1852 AAAACCGCTTGCAGACACAGAGATAGAAATGTTTGGAGAGAGAGTGGCTGTTGCA 1911
 Db 1801 AAAACCGCTTGCAGACACAGAGATAGAAATGTTTGGAGAGAGAGTGGCTGTTGCA 1860
 Qy 1912 AATGTTTCTTTTATATGTTTCTGATATGCTGATGCTGATGCTGATATTTGATTT 1971
 Db 1861 AATGTTTCTTTTATATGTTTCTGATATGCTGATGCTGATGCTGATATTTGATTT 1920
 Qy 1972 AAAATCTTTCCTTCCGAGTGAATATACAGACAAATGATCTTCCGTGATAGATT 2031
 Db 1921 AAAATCTTTCCTTCCGAGTGAATATACAGACAAATGATCTTCCGTGATAGATT 1980
 Qy 2032 TTTTCTTCCAGTTTACAGTGTGTTGAATCCATCTCTATATCTGACAAACCACTTT 2091
 Db 1981 TTTTCTTCCAGTTTACAGTGTGTTGAATCCATCTCTATATCTGACAAACCACTTT 2040
 Qy 2092 TTTAAGACAGTTGAAACAGCTGCTGCAAAACATCAGAGAAATCAATTTTCAAAAT 2151
 Db 2041 TTTAAGACAGTTGAAACAGCTGCTGCAAAACATCAGAGAAATCAATTTTCAAAAT 2100
 Qy 2152 AAAAAAAGTTTATCTACATCCATGTTGATAGAGAGTCTCTTCCCTGAAACTT 2211
 Db 2101 AAAAAAAGTTTATCTACATCCATGTTGATAGAGAGTCTCTTCCCTGAAACTT 2160
 Qy 2212 GGGGTTTTGAACAAATATACCTTGAAGACAGTATATGAAACAGTTTCTAG 2265
 Db 2161 GGGGTTTTGAACAAATATACCTTGAAGACAGTATATGAAACAGTTTCTAG 2214

RESULT 5
 US-09-928-175-6
 ; Sequence 6, Application US/09928175
 ; Patent No. US20020123618A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Paszcy, Christopher J.
 ; APPLICANT: Gong, Jianhua
 ; APPLICANT: Daugherty, Betsy
 ; APPLICANT: Rogers, No. US20020123618A1ma
 ; TITLE OF INVENTION: Leucine-Rich G Protein Coupled Receptor-8 Molecules and
 ; TITLE OF INVENTION: Uses Thereof
 ; FILE REFERENCE: 00-1229
 ; CURRENT APPLICATION NUMBER: US/09/928,175
 ; CURRENT FILING DATE: 2001-08-10
 ; PRIOR APPLICATION NUMBER: 60/224,455
 ; PRIOR FILING DATE: 2000-08-10
 ; NUMBER OF SEQ ID NOS: 42
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 6
 ; LENGTH: 2193
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(2190)
 ; NAME/KEY: s19_peptide
 ; LOCATION: (1)..(108)
 US-09-928-175-6

Query Match 93.2%; Score 2111; DB 10; Length 2193;
 Best Local Similarity 96.8%; Pred. No. 0;
 Matches 2193; Conservative 0; Mismatches 0; Indels 72; Gaps 1;
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 Db 1 ATGATGTTTCTGCTGTTTAAACATCTCTTCAAGCTGATGATTAACATGTTCTTT 60
 Qy 61 CTACTTCATTTATGCTTCTGATCATATGCAAGATTTTGCATGCTGAAGTATACATG 120

Db 61 CTACTTCATTTCTGATCTGATCAATGTCAGAAATTTTGACCTGATCTCAAGTAGCATG 120
Qy 121 ATCACTCCCTTCATGCGCAAAAGATATTTTCCCTGCGGAAATCTTACCAAGTCTTACC 180
Db 121 ATCACTCCCTTCATGCGCAAAAGATATTTTCCCTGCGGAAATCTTACCAAGTCTTACC 180
Qy 181 CGAGCTTTTCATCTGATGCGCAAGATGACTGTGGAAACGGGGCGGACGAAAGAACTGT 240
Db 181 CGAGCTTTTCATCTGATGCGCAAGATGACTGTGGAAACGGGGCGGACGAAAGAACTGT 240
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Db 241 GGTGCACTAGTGTGATGGGCGGACATATTTGGCACTGATGCAAGAAATGCTAACGCGTG 300
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Db 301 GCCTTAACACAGAGTCTTTCTTAAACAGTATCCACATGCTGTGACTGCAAGAAACT 360
Qy 361 GAATTTGAATGTGTAATGTGATCTTAAAGTCTGTGCGGATGATTTCTAACATGTGACA 420
Db 361 GAATTTGAATGTGTAATGTGATCTTAAAGTCTGTGCGGATGATTTCTAACATGTGACA 420
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Db 421 TTACTGCTCTTAAAGAAACAAATCCACAGTCTTCCAGATTAAGTTTCTAACATATC 480
Qy 481 ACAAACTTAAAGATATTTCTGACATATGATGACATTAAGACATATCCAGAAAGCA 540
Db 481 ACAAACTTAAAGATATTTCTGACATATGATGACATTAAGACATATCCAGAAAGCA 540
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Db 541 TTTTGTGATTAATGTAATCTGCAAAATTTATATCTCAACACAGCTGATCAACACCTTC 600
Qy 601 AGACCTGGAATTTCAAGAACTTACATGCTTACCTGCTTAAATTTCTGATGATGACATCA 660
Db 601 AGACCTGGAATTTCAAGAACTTACATGCTTACCTGCTTAAATTTCTGATGATGACATCA 660
Qy 661 ATTAACAGAAATTTCAAGGCTTGTGTTACGGGATTAATTTCTGTTTCTGCTATG 720
Db 661 ATTAACAGAAATTTCAAGGCTTGTGTTACGGGATTAATTTCTGTTTCTGCTATG 720
Qy 721 GTTAATTAATCTTGAAGCTCTTCCAGACAGATGTGCGCAATGCTCAACTCAAC 780
Db 721 GTTAATTAATCTTGAAGCTCTTCCAGACAGATGTGCGCAATGCTCAACTCAAC 780
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Db 781 TGGGTGGAATTTGGAAGGCAATGAATTAAGTATCTCAAAATTTCTGATGCTGCTG 840
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Db 841 GATTCGCTCACAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
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Qy 961 TCACCTCACCTTTTAAAGCTTGAAGCTTCTCAAAAGCTGAACTGTGATCTCAATCTCT 1020
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Db 1021 CTATGATATCTTCAAGAAACAGTTTGAAGCTTAAACAACTTCAAGTCTGAGCTG 1080
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Db 1201 CACATTTATTTCAAAACCTTGTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260

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Db 1381 GATTCGCTGATGAGGATTTTCAATCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
Qy 1441 CAGTATCAGAAATATGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
Db 1441 CAGTATCAGAAATATGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1500
Qy 1501 CTGGCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
Db 1501 CTGGCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560
Qy 1561 TTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1620
Db 1561 TTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1620
Qy 1621 ATCTGATTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
Db 1621 ATCTGATTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1680
Qy 1681 GATTAATTTGAAATCTTAAAGGAAATGAGGATTTTCAATGCTGCTGCTGCTGCTGCTGCTG 1740
Db 1681 GATTAATTTGAAATCTTAAAGGAAATGAGGATTTTCAATGCTGCTGCTGCTGCTGCTGCTG 1740
Qy 1741 ACAGAAATTTGAAAGGAAATGAGGATTTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1800
Db 1741 ACAGAAATTTGAAAGGAAATGAGGATTTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1800
Qy 1801 GCTTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1860
Db 1801 GCTTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1860
Qy 1861 TTTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1920
Db 1861 TTTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1920
Qy 1921 TTTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1980
Db 1921 TTTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1980
Qy 1981 TTTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2040
Db 1981 TTTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2040
Qy 2041 TTTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2100
Db 2041 TTTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2100
Qy 2101 TTTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2160
Db 2101 TTTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2160
Qy 2161 TTTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2220
Db 2161 TTTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2220
Qy 2221 TTTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2280
Db 2221 TTTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2280
Qy 2281 TTTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2340
Db 2281 TTTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2340

RESULT 6
US-09-965-536A-5
Sequence 5, Application US/0965536A
Publication No. US2003027323A1
GENERAL INFORMATION:
APPLICANT: FEDER, J. N.
APPLICANT: MINTER, G.
APPLICANT: RAMANATHAN, C. S.
APPLICANT: HAWKEN, D. R.
TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGRBRMYS,
TITLE OF INVENTION: EXPRESSED HIGHLY IN BRAIN AND OVARIAN TISSUES
FILE REFERENCE: D0041NP
CURRENT APPLICATION NUMBER: US/09/965,536A
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/235,713
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: 60/261,781
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: 60/306,605
PRIOR FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: 60/310,436
PRIOR FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 2142
TYPE: DNA
ORGANISM: Homo sapiens
US-09-965-536A-5

Query Match 90.9%; Score 2060; DB 11; Length 2142;

Best Local Similarity 96.7%; Pred. No. 0; Mismatches 0; Indels 72; Gaps 1;

Matches 2142; Conservative 0; Mismatches 0; Indels 72; Gaps 1;

QY 52 ATGTTCTTTCTACTTCAATTCATTCGTTCTGATCAATGCAAGATTTTGGCACTGACTCA 111
DB 1 ATGTTCTTTCTACTTCAATTCATTCGTTCTGATCAATGCAAGATTTTGGCACTGACTCA 60
QY 112 GGTGACATGATCACTCTCTTATGCAAAAGATTTTCCCTGCGGAACTTTACCAAG 171
DB 61 GGTGACATGATCACTCTCTTATGCAAAAGATTTTCCCTGCGGAACTTTACCAAG 120
QY 172 TGTCTACCCGAGCTTTTCACTGATGCAAGATGACTGTGGAAACGGGCGGAGAA 231
DB 121 TGTCTACCCGAGCTTTTCACTGATGCAAGATGACTGTGGAAACGGGCGGAGAA 180
QY 232 GAGAACTGTGTGACACTAGTGTGATGGCGACATATTTGGCAAGTGAATGCT 291
DB 181 GAGAACTGTGTGACACTAGTGTGATGGCGACATATTTGGCAAGTGAATGCT 240
QY 292 AACAGCTGTGCTTAAACAGAGAGTCTTTCTTAAACAGATTCACAAATGCTGATGC 351
DB 241 AACAGCTGTGCTTAAACAGAGAGTCTTTCTTAAACAGATTCACAAATGCTGATGC 300
QY 352 AAAGAACTGAATGTGAATGTGAATGTGAATGTGAATGTGAATGTGAATGTGAATGTGA 411
DB 301 AAAGAACTGAATGTGAATGTGAATGTGAATGTGAATGTGAATGTGAATGTGAATGTGA 360
QY 412 AATGTGACTTACTGTCTCTTAAAGAAACAAATTCACAGTCTTCCAGATTAAGTTTTC 471
DB 361 AATGTGACTTACTGTCTCTTAAAGAAACAAATTCACAGTCTTCCAGATTAAGTTTTC 420
QY 472 ATCAATACACAAATCTTAAAGATTAATTTCTGAGATTAATTTGATTAAGATTAATTTTC 531
DB 421 ATCAATACACAAATCTTAAAGATTAATTTCTGAGATTAATTTGATTAAGATTAATTTTC 480
QY 532 AGGAAGCATTTTGTGATTAATGTGAATGTGAATGTGAATGTGAATGTGAATGTGAATGTGA 591
DB 481 AGGAAGCATTTTGTGATTAATGTGAATGTGAATGTGAATGTGAATGTGAATGTGAATGTGA 517
QY 592 AGAAGCTGAGACTGTGAATGTGAATGTGAATGTGAATGTGAATGTGAATGTGAATGTGA 651
|||||

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DB 529 GACATTCACAAATTCACAGAGCTTTGTTACGGATTAATTTCTGTTTTC 588
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DB 589 CTGTCTATGTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 648
QY 772 CAATCACTGTGTGTGATTTGAGAGCAATAGATTAATTAATTAATTAATTAATTAATTAATTA 831
DB 649 CAATCACTGTGTGTGATTTGAGAGCAATAGATTAATTAATTAATTAATTAATTAATTAATTA 708
QY 832 CTGTGTGTGATTTGCTCAAGTGTGTTTCTGCTAGAAATCAATTTGTTTTC 891
DB 709 CTGTGTGTGATTTGCTCAAGTGTGTTTCTGCTAGAAATCAATTTGTTTTC 768
QY 892 GAGAAACATTTTCTTCAATTAATAAATTTAGAGAACTGATCTGTCAATAGATA 951
DB 769 GAGAAACATTTTCTTCAATTAATAAATTTAGAGAACTGATCTGTCAATAGATA 828
QY 952 ACGAGCTATCACTTCACTTTTAAAGACTTGAAGCTTCAAAAGCTGAACCTGTCA 1011
DB 829 ACGAGCTATCACTTCACTTTTAAAGACTTGAAGCTTCAAAAGCTGAACCTGTCA 888
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DB 889 TCCATCTCTTATGTATCTTCAAGAAACCAAGTTGAAGCTTAAACCTTCACTGTCT 948
QY 1072 CTAGACCTGAAAGATTAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1131
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DB 1069 ATATGATGATCCCTTGAACGAGCAATTTCTTCAATTTAGAGAACTTGTGCTAAATATC 1128
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DB 1129 CTCAGAAATTTGTCTGAGTTATAGCTTTCATTAACCTGCTTGAATCTTTTGTCTAT 1188
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DB 1189 GGCATGATCTTTCTTAAAGCTGAATAATCACTACAGCTATGTCATCAAAATCTT 1248
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DB 1249 TGTGTGCTGATTTGCTGATGAGGTTTATCTTGTGTTGGCAATTTTGCATTAATA 1308
QY 1432 TACCGAGGACATGATGAGATTAATGCTTGTGTGATGAGAGGCTGAGTCCGCTTC 1491
DB 1309 TACCGAGGACATGATGAGATTAATGCTTGTGTGATGAGAGGCTGAGTCCGCTTC 1368
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DB 1369 ATGGAGTCTGTGCTATGCTGTCACACCGAAGTCTGCTGATGATGATGATGATGATGATGAT 1428
QY 1552 TTGAGAAAGTCTGTGCTATGCTTCCCTTCAATTAATTAATTAATTAATTAATTAATTAATTA 1611
DB 1429 TTGAGAAAGTCTGTGCTATGCTTCCCTTCAATTAATTAATTAATTAATTAATTAATTAATTA 1488
QY 1612 ACTCACTGATCTGATTTGATCTGATGAGGCGGATTTTAAATTAATTAATTAATTAATTAATTA 1671
DB 1489 ACTCACTGATCTGATTTGATCTGATGAGGCGGATTTTAAATTAATTAATTAATTAATTAATTA 1548
QY 1672 TGAATTAAGATTAATTTGAGAACTTTATGAGAAATTAATTAATTAATTAATTAATTAATTAATTA 1731
DB 1549 TGAATTAAGATTAATTTGAGAACTTTATGAGAAATTAATTAATTAATTAATTAATTAATTAATTA 1608
|||||

QY 1732 TATGACAAACAGAAATATGGAAGCAAGGATTTCTTGGAAATTTTCTAGGTG 1791
DB 1609 TATACCAACAGAAAGATATGGAAGCAAGGATTTCTTGGAAATTTTCTAGGTG 1668
QY 1792 AACTGCTGCTTTCTCATCATGTGTGTTTCTATATTAATTAATGTTCTGTTCAATCAA 1851
DB 1669 AACTGCTGCTTTCTCATCATGTGTGTTTCTATATTAATTAATGTTCTGTTCAATCAA 1728
QY 1852 AAAACCGCTTGCAGACCAAGATGAAATGTTTGAAGAGAGAGGTGCTGTTGCA 1911
DB 1729 AAAACCGCTTGCAGACCAAGATGAAATGTTTGAAGAGAGGTGCTGTTGCA 1788
QY 1912 AATGCTTTCTTTTATATGTTCTGTGATGCAATGCTGCTGATTTCTGTAATTTGAGTT 1971
DB 1789 AATGCTTTCTTTTATATGTTCTGTGATGCAATGCTGCTGATTTCTGTAATTTGAGTT 1848
QY 1972 AAAATCTTTTCCCTCTTCCGGGTGGAATATCCAGACAAATGACTTCTGATATGATTT 2031
DB 1849 AAAATCTTTTCCCTCTTCCGGGTGGAATATCCAGACAAATGACTTCTGATATGATTT 1908
QY 2032 TTTTTCCTTCCAGTTAAAGATGCTTTGAATCAATCCTCTATATCTGACAAACCACTTT 2091
DB 1909 TTTTTCCTTCCAGTTAAAGATGCTTTGAATCAATCCTCTATATCTGACAAACCACTTT 1968
QY 2092 TTTAAGACAAAGTTGAAACAGCTGCTGACAAACATCAGAGAAATCAATTTTCAAAAT 2151
DB 1969 TTTAAGACAAAGTTGAAACAGCTGCTGACAAACATCAGAGAAATCAATTTTCAAAAT 2028
QY 2152 AAAAAAAGATTTATCTACATCCATTTGTGTGATATGAGAGACTCTCTTCCCTGAAATTT 2211
DB 2029 AAAAAAAGATTTATCTACATCCATTTGTGTGATATGAGAGACTCTCTTCCCTGAAATTT 2088
QY 2212 GGGGTTTGAACAAATATACACTTGGAGACAGTATATGAAACGATTTCTAG 2265
DB 2089 GGGGTTTGAACAAATATACACTTGGAGACAGTATATGAAACGATTTCTAG 2142

RESULT 7

US-09-928-175-11
Sequence 11, Application US/09928175
Patent No. US20020123618A1
GENERAL INFORMATION:
APPLICANT: Paszty, Christopher J.
APPLICANT: Gong, Jianhua
APPLICANT: Daugherty, Betsy
APPLICANT: Rogers, No. US20020123618A1ma
TITLE OF INVENTION: Leucine-Rich G Protein Coupled Receptor-8 Molecules and
FILE REFERENCE: 00-1229
CURRENT APPLICATION NUMBER: US/09/928,175
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/224,455
PRIOR FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patent Ver. 2.0
SEQ ID NO 11
LENGTH: 2049
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(2046)
NAME/KEY: sig_peptide
LOCATION: (1)..(108)
US-09-928-175-11

Query Match 79.6%; Score 1803; DB 10; Length 2049;
Best Local Similarity 90.5%; Pred. No. 0;
Matches 2049; Conservative 0; Mismatches 0; Indels 216; Gaps 3;

QY 1 ATGATGTTTTCCTGTTTTTAAACATCTTCAGCTCAGATGATTAACATGTTCTT 60
|||||

DB 1 ATGATGTTTTCCTGTTTTTAAACATCTTCAGCTCAGATGATTAACATGTTCTT 60
QY 61 CTAATTCATTCATGCTTGTGATCAATGTCAAAGATTTTGCATGATCAAGATGATG 120
DB 61 CTAATTCATTCATGCTTGTGATCAATGTCAAAGATTTTGCATGATCAAGATGATG 120
QY 121 ATCACTCTTCATGTCACAAAAGATATTTTCCCTGTGGAAATCTTACAAAGTCTTACC 180
DB 121 ATCACTCTTCATGTCACAAAAGATATTTTCCCTGTGGAAATCTTACAAAGTCTTACC 180
QY 181 CGAGCTTTTCACTGTATGTCAGAGATGATCTGTGGAAACGGGGGCGAGCAAGAGACTGT 240
DB 181 CGAGCTTTTCACTGTATGTCAGAGATGATCTGTGGAAACGGGGGCGAGCAAGAGACTGT 240
QY 241 GGTACACTAGTGGATGGGCAACATATTTGGCACTGTGAGAAATGCTTACAGCGTG 300
DB 241 GGTACACTAGTGGATGGGCAACATATTTGGCACTGTGAGAAATGCTTACAGCGTG 300
QY 301 GCCTTAAACAGAGAGCTTTCTTAAACAGTATCCAAATGCTGTGACTGCAAGAAACT 360
DB 301 GCCTTAAACAGAGAGCTTTCTTAAACAGTATCCAAATGCTGTGACTGCAAGAAACT 360
QY 361 GAATTTGAATGTGTAATATGATGCTTAAAGTCTGTGCGATGATTTTCTTAAACATGTA 420
DB 361 GAATTTGAATGTGTAATATGATGCTTAAAGTCTGTGCGATGATTTTCTTAAACATGTA 420
QY 421 TTAATGCTCTTAAAGAAACAAATATCCAGTCTTCAGATTAAGTTTCAATCAATATAC 480
DB 421 TTAATGCTCTTAAAGAAACAAATATCCAGTCTTCAGATTAAGTTTCAATCAATATAC 480
QY 481 ACAAACTTAAAGATATTTCTTACAGATATATGATATGACACATATCCAGAGAAAGCA 540
DB 481 ACAAACTTAAAGATATTTCTTACAGATATATGATATGACACATATCCAGAGAAAGCA 540
QY 541 TTTTGTGATGATGATATGTCGAAATATATATATCAACCAACATGATCAACACCTC 600
DB 541 TTTTGTGATGATGATATGTCGAAATATATATATCAACCAACATGATCAACACCTC 600
QY 601 AGACCTGGAATATTCAAAGACTTACATCAGCTAACCTTGGCTAATTCAGATGACATCCA 660
DB 601 AGACCTGGAATATTCAAAGACTTACATCAGCTAACCTTGGCTAATTCAGATGACATCCA 660
QY 661 ATAAACGAATTTCAACAGCGCTGTTTACCGGATTAATTCCTGTTTCTGTCTATG 720
DB 661 ATAAACGAATTTCAACAGCGCTGTTTACCGGATTAATTCCTGTTTCTGTCTATG 720
QY 721 GTTAATTAACATTAAGAGCTTCCCAAGAGATGTGCGCCAAAGCCCACTCAAC 780
DB 721 GTTAATTAACATTAAGAGCTTCCCAAGAGATGTGCGCCAAAGCCCACTCAAC 780
QY 781 TGGGTGATTTGGAAGCAATAGAAATTAAGATCTCACAATTTCTAGCTTCTGTCTG 840
DB 781 TGGGTGATTTGGAAGCAATAGAAATTAAGATCTCACAATTTCTAGCTTCTGTCTG 840
QY 841 GATTCGCTCACAGTCTGTTTCTGCTTGAATCAAAATGTTTGTTCAGAGAAAGCA 900
DB 841 GATTCGCTCACAGTCTGTTTCTGCTTGAATCAAAATGTTTGTTCAGAGAAAGCA 900
QY 901 TTTTCTTCATTAATAAATTTAGAGAACTGATCTGTAGCAATAGATTAACGAGCTA 960
DB 901 TTTTCTTCATTAATAAATTTAGAGAACTGATCTGTAGCAATAGATTAACGAGCTA 960
QY 961 TCACCTCACTTTTAAAGATTAAGATTTTCAAAAAGCTGAACTGTCTATCCATCTCT 1020
DB 961 TCACCTCACTTTTAAAGATTAAGATTTTCAAAAAGCTGAACTGTCTATCCATCTCT 1020
QY 1021 CTTATGATCTTCAACAAAGCAAGTTGAAGTCTTAAACCACTTCACTCTGACCTG 1080
DB 1021 CTTATGATCTTCAACAAAGCAAGTTGAAGTCTTAAACCACTTCACTCTGACCTG 1080
QY 1081 GAAAGATAGAGATTTCCAAATATTAACACAGATGTTTCAACCAAGATATCTTCT 1140
DB 1081 GAAAGATAGAGATTTCCAAATATTAACACAGATGTTTCAACCAAGATATCTTCT 1140
QY 1140 GAAAGATAGAGATTTCCAAATATTAACACAGATGTTTCAACCAAGATATCTTCT 1200
DB 1140 GAAAGATAGAGATTTCCAAATATTAACACAGATGTTTCAACCAAGATATCTTCT 1200


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Db      774  TTTGGCTGCTAATTTAGATGACAAACCGATCACCAGATCTCACAAGAGCTTTATAG 833
Qy      692  GATTAATTCCTTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCT 751
Db      834  GGTTAACCTCTTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCT 893
Qy      752  AGATGTGTCCCAATGCTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 811
Db      894  CATGTGTGTCTCAATGCTCACTCACTCACTCACTCACTCACTCACTCACTCACTCA 953
Qy      812  ATCTCACAATTTCACTGTTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 871
Db      954  ACATAAGCAATCCACCTTCTTAACGTGCACTGCTCACTGCTGCTGCTGCTGCTGCT 1013
Qy      872  ATCAATTTGTTTGTTCAGAGAAAGATTTTCTTCACTTAAATAATTTAGAGAACTGG 931
Db      1014  ATCAATTTGTTTGTTCAGAGAAAGATTTTCTTCACTTAAATAATTTAGAGAACTGG 1073
Qy      932  ATCTGTAGCAATACGATAAGAGAGATCACTCACTCACTCACTCACTCACTCACTCACT 991
Db      1074  ACCTGTAGCAATACGATAAGAGAGATTTTCTTCACTTAAATAATTTAGAGAACTGG 1133
Qy      992  TACAAAAGCTGACCTGTATCTCACTCTTTATGTATCTTCACTCACTCACTCACTCA 1051
Db      1134  TCCGAAAGCTGACCTGTATCTCACTCTTGTATGTATCTCACTCACTCACTCACTCA 1193
Qy      1052  GTCTTAAACAATTCAGTCTCTAGACCTGAAAGAGATGAGATTCGAATTTAAACACAC 1111
Db      1194  GTCTCAAAACAATTCAGTCTCTAGACCTGAAAGAGATGAGATTTCAAAACATTAAGCA 1253
Qy      1112  GAATGTTTCAACCCATGAGAGATCTTTCTCACTTATTTCAAAAACCTTGTGATCTCT 1171
Db      1254  GAATGTTTCAACCCATGAGAGATCTTTCTCACTTATTTGAAAACCTTGTGATCTCT 1313
Qy      1172  CCTATGCTCCCAATGCTGAGATGATGATGATGATGATGATGATGATGATGATGATG 1231
Db      1314  CCTATGCTCCCAATGCTGAGATGATGATGATGATGATGATGATGATGATGATGATG 1373
Qy      1232  ACCTTTGGCTAACAATTCCTCAAGATTTTGTGAGATTTTGTGAGATTTTGTGAGAT 1291
Db      1374  ACCTTTGGCTAACAATTCCTCAAGATTTTGTGAGATTTTGTGAGATTTTGTGAGAT 1433
Qy      1292  TTGGAATCTTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1351
Db      1434  TTGGAATCTTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1493
Qy      1352  CTATGTCCATCAAAATCTTTTGTGATGATGATGATGATGATGATGATGATGATGAT 1411
Db      1494  CTATGTCCATCAAAATCTTTTGTGATGATGATGATGATGATGATGATGATGATGAT 1553
Qy      1412  TTGGAATCTTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1471
Db      1554  TGGGGCTTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1613
Qy      1472  AGAGGTGCAAGTGCCTGCTCATGAGGATTCCTGAGCATGCTGCAACGAGCTCTGTC 1531
Db      1614  AGAGGTGCAAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1673
Qy      1532  TGCTAATGACCTGATCTTGTGAGAGATTCCTGATGATGATGATGATGATGATGATG 1591
Db      1674  TGCTAATGACCTGATCTTGTGAGAGATTCCTGATGATGATGATGATGATGATGATG 1733
Qy      1592  TTGCACTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1651
Db      1734  TGGGGCTTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1793
Qy      1652  TAAATGCTGATATTCATTTTGTGAGATTAAGATTTTGTGAGATTTTGTGAGATTA 1711
Db      1794  TCAATGCGGCGCTTCCGTTACACAGAGAGATTTTGTGAGATTTTGTGAGATTA 1853
Qy      1712  GAGTATGTTTCCATTTATATATGACCAAGAGATTTTGTGAGATTTTGTGAGATTA 1771

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Db      1854  GAGTGTGCTTCCACCTTATATGACCAAGAGATTTTGTGAGATTTTGTGAGATTTCC 1913
Qy      1772  TTGGAATTTCTAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1831
Db      1914  TTGGAATTTCTAGAGATGATGATGATGATGATGATGATGATGATGATGATGATG 1973
Qy      1832  CTATGTCTGTTCCATTCAAAACCCGCTTGTGAGAGAGAGAGAGAGAGAGAGAGAG 1891
Db      1974  CAAATGTTCTGCTCAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2033
Qy      1892  GAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1951
Db      2034  GGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2093
Qy      1952  GGAATTCCTGATTTGTGATTAAGATTTTCTTCCCTGCTGCTGCTGCTGCTGCTGCT 2011
Db      2094  GGAATTCCTGATTTGTGATTAAGATTTTCTTCCCTGCTGCTGCTGCTGCTGCTGCT 2153
Qy      2012  TGAATTCCTGATTTGTGATTAAGATTTTCTTCCCTGCTGCTGCTGCTGCTGCTGCT 2071
Db      2154  TGAATTCCTGATTTGTGATTAAGATTTTCTTCCCTGCTGCTGCTGCTGCTGCTGCT 2213
Qy      2072  ATACTCTCAACAACCTTTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2131
Db      2214  AACTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2273
Qy      2132  GGAATTCATTTTCAAAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2191
Db      2274  GGAATTCATTTTCAAAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2253
Qy      2192  ACTCTCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2251
Db      2234  A--GTCTTCACTTAACCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2390
Qy      2252  AACGAGTTTC 2262
Db      2391  AGCGGTCTCC 2401

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RESULT 9

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US-09-928-175-19
; Sequence 19, Application US/09928175
; Patent No. US200213618A1
; GENERAL INFORMATION:
; APPLICANT: Paszty, Christopher J.
; APPLICANT: Gong, Jianhua
; APPLICANT: Daugherty, Betsy
; TITLE OF INVENTION: Leucine-Rich G Protein Coupled Receptor-8 Molecules and
; FILE REFERENCE: 00-1229
; CURRENT APPLICATION NUMBER: US/09/928,175
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/224,455
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 19
; LENGTH: 2214
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) ..(2211)
; NAME/KEY: sig_peptide
; LOCATION: (1) ..(57)
US-09-928-175-19

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Query Match      69.7%; Score 1579; DB 10; Length 2214;
Best Local Similarity 82.5%; Pred. No. 0;
Matches 1823; Conservative 0; Mismatches 365; Indels 3; Gaps 1;
Qy      52  ATGTTCTTTCTTCAATTTCAATGATGATGATGATGATGATGATGATGATGATGATG 111

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RESULT 10
US-09-928-175-4
Sequence 4, Application US/09928175
Patent No. US20020123618A1
GENERAL INFORMATION:
APPLICANT: Paszty, Christopher J.
APPLICANT: Gong, Jianhua
APPLICANT: Daugherty, Betsy
APPLICANT: Rogers, No. US20020123618A1ma
TITLE OF INVENTION: Leucine-Rich G Protein Coupled Receptor-8 Molecules and
FILE REFERENCE: 00-1229
CURRENT APPLICATION NUMBER: US/09/928,175
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/224,455
PRIOR FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 1149
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1) .. (1149)
US-09-928-175-4
Query Match
Blast Local Similarity 50.7%; Score 1149; DB 10; Length 1149;
Matches 1149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 109 CAAGTAGCATGATCACTCTTCATGCGCAAAAAGATATTTCCCTGTGGATCTTACC 168
DB 1 CAAGTAGCATGATCACTCTTCATGCGCAAAAAGATATTTCCCTGTGGATCTTACC 60
QY 169 AAGTGTTCACCCGAGCTTTTCACTGTGATGCGAAGATGATCTGTGGAAACGGGCGGAC 228
DB 61 AAGTGTTCACCCGAGCTTTTCACTGTGATGCGAAGATGATCTGTGGAAACGGGCGGAC 120
QY 229 GAAGAGAACTGTGTGACACTAGTGTGATGGGCGACATTTTGGCACTGTGATGGAAT 288
DB 121 GAAGAGAACTGTGTGACACTAGTGTGATGGGCGACATTTTGGCACTGTGATGGAAT 180
QY 289 GCTAACAGCGTGCCCTTAAACAGAGAGCTCTTCTTAAACAGATTCACATGCTGTGAC 348
DB 181 GCTAACAGCGTGCCCTTAAACAGAGAGCTCTTCTTAAACAGATTCACATGCTGTGAC 240
QY 349 TGCAGAAAGAACTGATTTGAATGTGTAATGTGACTTAAAGTCTGTGCGCATGATTTCT 408
DB 241 TGCAGAAAGAACTGATTTGAATGTGTAATGTGACTTAAAGTCTGTGCGCATGATTTCT 300
QY 409 AACAAATGTACATTAAGTCTCTTAAAGAAAACAAATCCACAGCTTCCAGATTAAGTT 468
DB 301 AACAAATGTACATTAAGTCTCTTAAAGAAAACAAATCCACAGCTTCCAGATTAAGTT 360
QY 469 TTCATCAATATACCAAAATCTTAAAGATATTTCTTACAGATTAATGATAGACATA 528
DB 361 TTCATCAATATACCAAAATCTTAAAGATATTTCTTACAGATTAATGATAGACATA 420
QY 529 TCCAGAGAAAGCATTTTGTGATTAATGTGCAAAATATTAATTCACACCAACATGTC 588
DB 421 TCCAGAGAAAGCATTTTGTGATTAATGTGCAAAATATTAATTCACACCAACATGTC 480
QY 589 ATCAACAACCTGAGACTGGAATATTCAGAACTTACATCAGCTTACCTGGGTAATTTCA 648
DB 481 ATCAACAACCTGAGACTGGAATATTCAGAACTTACATCAGCTTACCTGGGTAATTTCA 540
QY 649 GATGACAAATCAATAACAGAAATTTTACAGCGCTTGTTTACGGGATTAATTCCTTGT 708
DB 541 GATGACAAATCAATAACAGAAATTTTACAGCGCTTGTTTACGGGATTAATTCCTTGT 600

QY 709 TTCTGTCTATGTTAATACTTACATTAAGACCTTTCCCAAGCAGATGTGTGCCAATG 768
DB 601 TTCTGTCTATGTTAATACTTACATTAAGACCTTTCCCAAGCAGATGTGTGCCAATG 660
QY 769 CCTCAACTCACTGGGATTTGGAAGGCAATGAATTAAGTATCTCAGAAATCTTACG 828
DB 661 CCTCAACTCACTGGGATTTGGAAGGCAATGAATTAAGTATCTCAGAAATCTTACG 720
QY 829 TTCTGTCTATGTTAATACTTACATTAAGACCTTTCCCAAGCAGATGTGTGCCAATG 888
DB 721 TTCTGTCTATGTTAATACTTACATTAAGACCTTTCCCAAGCAGATGTGTGCCAATG 780
QY 889 CCAAGAGACATTTTCTTCAATTAATAATTTAGAGACTGATCTGTCTAGCAATGCG 948
DB 781 CCAAGAGACATTTTCTTCAATTAATAATTTAGAGACTGATCTGTCTAGCAATGCG 840
QY 949 ATTAAGGAGATATCACTTCACTTTTAAAGACTTGAAGCTTCAAAAGCTGACCTG 1008
DB 841 ATTAAGGAGATATCACTTCACTTTTAAAGACTTGAAGCTTCAAAAGCTGACCTG 900
QY 1009 TCATCAATCTCTTATGATCTTCAACAGACAGATTTGAAGCTTAAACAACTTACG 1068
DB 901 TCATCAATCTCTTATGATCTTCAACAGACAGATTTGAAGCTTAAACAACTTACG 960
QY 1069 TCTCTAGACCTGGAAGGATGAGATTCGAATTAATAACAGCAATGTTTCAACCTATG 1128
DB 961 TCTCTAGACCTGGAAGGATGAGATTCGAATTAATAACAGCAATGTTTCAACCTATG 1020
QY 1129 AAGATCTTCTCACTTATTAATTTCAAAACCTTGAATCTGCTATGCTCCCATGTC 1188
DB 1021 AAGATCTTCTCACTTATTAATTTCAAAACCTTGAATCTGCTATGCTCCCATGTC 1080
QY 1189 CGAATATGATGCTTACAGGACGCAATTTCTTCAATTTAGAGACTTGTGGCTTAACAT 1248
DB 1081 CGAATATGATGCTTACAGGACGCAATTTCTTCAATTTAGAGACTTGTGGCTTAACAT 1140
QY 1249 ATCTTCAGA 1257
DB 1141 ATCTTCAGA 1149
RESULT 11
US-10-321-807-17
Sequence 17, Application US/10321807
Patent No. US20030166148A1
GENERAL INFORMATION:
APPLICANT: Dang, Huong T.
APPLICANT: Lowitz, Kevin P.
TITLE OF INVENTION: No. US20030166148A1-Endogenous, Constitutively Activated Human G
FILE REFERENCE: AREN0086
CURRENT APPLICATION NUMBER: US/10/321,807
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: US/09/714,008
PRIOR FILING DATE: 2000-11-16
PRIOR APPLICATION NUMBER: 09/170,496
PRIOR FILING DATE: 1999-11-17
PRIOR APPLICATION NUMBER: PCT/US99/23938
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: 60/166,088
PRIOR FILING DATE: 1999-11-17
PRIOR APPLICATION NUMBER: 60/166,099
PRIOR FILING DATE: 1999-11-17
PRIOR APPLICATION NUMBER: 60/166,369
PRIOR FILING DATE: 1999-11-17
PRIOR APPLICATION NUMBER: 60/171,902
PRIOR FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 60/171,901
PRIOR FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 60/171,900
PRIOR FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 60/181,749


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Qy 529 TCACGAAAGCATTTTGGATTATGTAATCGCAATATTAATCTCAACCAACTGC 588
Db 421 TCACGAAAGCATTTTGGATTATGTAATCGCAATATTAATCTCAACCAACTGC 480
Qy 589 ATCAACACCCCTCAGCCGGAATATTCAAAGACTAGCTAGCTTGGCTAATCTTA 648
Db 481 ATCAACACCCCTCAGCCGGAATATTCAAAGACTAGCTAGCTTGGCTAATCTTA 540
Qy 649 GATGACATCCAAATTAACGAGATTTTCAGAGCGCTGTTCAGGGATTAATTCCTGTTT 708
Db 541 GATGACATCCAAATTAACGAGATTTTCAGAGCGCTGTTCAGGGATTAATTCCTGTTT 600
Qy 709 TTCTGCTATGTTAATTAATTAATTAAGCTTTCCCAAGCAGATGTGCCAAATG 768
Db 601 TTCTGCTATGTTAATTAATTAATTAAGCTTTCCCAAGCAGATGTGCCAAATG 660
Qy 769 CCTCAACTCACTGGTGGATTTTGGAAAGCAATGAATTAAGTATCTCAAAATTTCTACG 828
Db 661 CCTCAACTCACTGGTGGATTTTGGAAAGCAATGAATTAAGTATCTCAAAATTTCTACG 720
Qy 829 TTTCTGTCGTCGATTCGCTCAGAGTGTCTTCTGCTAGAAATCAAAATGTTTGT 888
Db 721 TTTCTGTCGTCGATTCGCTCAGAGTGTCTTCTGCTAGAAATCAAAATGTTTGT 747
Qy 889 CCAAGAAACATTTTCTTCAATTAATAAATTGAGAGACTGATCTGTCTAGCAATACG 948
Db 748 -----CTGATCTGTCTAGCAATACG 768
Qy 949 ATAAAGGAGTATCACTCAGCTTTTAAAGACTTGAAGCTTCAAAAGCTGAACCTG 1008
Db 769 ATAAAGGAGTATCACTCAGCTTTTAAAGACTTGAAGCTTCAAAAGCTGAACCTG 828
Qy 1009 TCATCAATCTCTTATGATCTTCAACAAGAACAGTTGAAAGCTTAAACAACTTCAG 1068
Db 829 TCATCAATCTCTTATGATCTTCAACAAGAACAGTTGAAAGCTTAAACAACTTCAG 888
Qy 1069 TCTCTAAGCTGGAAGGATGAGATTTCAAAATATTAACAAGATTTTCAACCCATG 1128
Db 889 TCTCTAAGCTGGAAGGATGAGATTTCAAAATATTAACAAGATTTTCAACCCATG 948
Qy 1129 AAGAATCTTCTCACTTATTTTCAAAAATTTGAGTCTGCTCTATGCTCCCATGTC 1188
Db 949 AAGAATCTTCTCACTTATTTTCAAAAATTTGAGTCTGCTCTATGCTCCCATGTC 1008
Qy 1189 CGAATATGATGCTCTGACGAGCGCATTTCTTCAATTTGAGACCTTGGCTTACAT 1248
Db 1009 CGAATATGATGCTCTGACGAGCGCATTTCTTCAATTTGAGACCTTGGCTTACAT 1068
Qy 1249 ATCTCTCAGA 1257
Db 1069 ATCTCTCAGA 1077

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RESULT 13
US-09-928-175-16
; Sequence 16, Application US/09928175
; Patent No. US20020123618A1
; GENERAL INFORMATION:
; APPLICANT: Paszty, Christopher J.
; APPLICANT: Gong, Jianhua
; APPLICANT: Daugherty, Betsy
; APPLICANT: Rogers, No. US20020123618A1ma
; TITLE OF INVENTION: Leucine-rich G Protein Coupled Receptor-8 Molecules and
; FILE REFERENCE: Uses Thereof
; CURRENT APPLICATION NUMBER: US/09/928,175
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/224,455
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 16
; LENGTH: 1101

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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1098)
; NAME/KEY: sig_peptide
; LOCATION: (1)..(108)
US-09-928-175-16

Query Match      43.8%; Score 991; DB 10; Length 1101;
Best Local Similarity 93.7%; Pred. No. 9,5e-251;
Matches 1073; Conservative 0; Mismatches 0; Indels 72; Gaps 1;

Qy 1 ATGATGTTTTCGTTTAAACATCTCTTCAAGCTCAGATGATTAACAATGTTCTTT 60
Db 1 ATGATGTTTTCGTTTAAACATCTCTTCAAGCTCAGATGATTAACAATGTTCTTT 60
Qy 61 CTACTTCAATTCATGTTTCTGATCAATGTCAAAGATTTTGGACTGACTCAAGTACATG 120
Db 61 CTACTTCAATTCATGTTTCTGATCAATGTCAAAGATTTTGGACTGACTCAAGTACATG 120
Qy 121 ATCACTGCTTCATGCAAAAAGATATTTTCCGTGGGAATCTTCAAGTGTCC 180
Db 121 ATCACTGCTTCATGCAAAAAGATATTTTCCGTGGGAATCTTCAAGTGTCC 180
Qy 181 CGAGCTTTTCACTGTGATGCGAAGATGACTGTGGGAACGGGCGGACGAAGAACTGT 240
Db 181 CGAGCTTTTCACTGTGATGCGAAGATGACTGTGGGAACGGGCGGACGAAGAACTGT 240
Qy 241 GGTGACACTAGTGGATGGGCGACATATTTGGCACAGTGCATGGAAATGCTAACAGCTG 300
Db 241 GGTGACACTAGTGGATGGGCGACATATTTGGCACAGTGCATGGAAATGCTAACAGCTG 300
Qy 301 GCCTTAACACGAGAGTCTTTCTTAAACAGATTCACAAGTCTGACTGCAAGAAACT 360
Db 301 GCCTTAACACGAGAGTCTTTCTTAAACAGATTCACAAGTCTGACTGCAAGAAACT 360
Qy 361 GAATGGAATGTGTAATGTTGATCTTAAAGTCTGTGCGATGATTTCTAACATGTGACA 420
Db 361 GAATGGAATGTGTAATGTTGATCTTAAAGTCTGTGCGATGATTTCTAACATGTGACA 420
Qy 421 TTAATGCTCTTAAGAAAAAACAATTCACAGTCTTCCAGTAATAGTTTCAATCAATAC 480
Db 421 TTAATGCTCTTAAGAAAAAACAATTCACAGTCTTCCAGTAATAGTTTCAATCAATAC 480
Qy 481 ACAAACTTAAAGATATTTCTCAGATTAATGCAATTGACATATCCAGGAAGCA 540
Db 481 ACAAACTTAAAGATATTTCTCAGATTAATGCAATTGACATATCCAGGAAGCA 540
Qy 541 TTTTGGATTAATGTAATCTGCAAAATTAATATCTCAACCAACATGCAACACCTC 600
Db 541 TTTTGGATTAATGTAATCTGCAAAATTAATATCTCAACCAACATGCAACACCTC 600
Qy 601 AGACCTGGAATATTCAAAGACTTACATCAGCTTAATCTGGAATTCAGAAAGCAATCCA 660
Db 601 AGACCTGGAATATTCAAAGACTTACATCAGCTTAATCTGGAATTCAGAAAGCAATCCA 660
Qy 661 ATAAACGAATTTTCAAGCGCTTTTACCGGATTAATTCCTGTTTCTCTGCTATG 720
Db 661 ATAAACGAATTTTCAAGCGCTTTTACCGGATTAATTCCTGTTTCTCTGCTATG 720
Qy 721 GTTAATAACTTACTTGAAGCTCTTCCCAAGCAGATGTGTGCCAAATGCTCAAC 780
Db 721 GTTAATAACTTACTTGAAGCTCTTCCCAAGCAGATGTGTGCCAAATGCTCAAC 780
Qy 781 TGGGTGATTTTGAAGCAATAGAAATTAAGTCTCAAAATTTAGCTTCTGTGTC 840
Db 781 TGGGTGATTTTGAAGCAATAGAAATTAAGTCTCAAAATTTAGCTTCTGTGTC 840
Qy 841 GATTCGCTCAGAGTGTCTTCTGCTAGAAATCAATGTTGTTTCCAGAGAAGACA 900
Db 841 GATTCGCTCAGAGTGTCTTCTGCTAGAAATCAATGTTGTTTCCAGAGAAGACA 855

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QY 901 TTTCTTCAATAAAATTTAGGAGAACTGATCTGCTAGCAATACGTAACGAGCTTA 960
DB 856 -----CTGGATCTGTCTAGCAATACGTAACGAGCTTA 888
QY 961 TCACCTCACCTTTTAAAGACTTGAAGCTTCTACAAAGCTGATCACTCAATCTCT 1020
DB 889 TCACCTCACCTTTTAAAGACTTGAAGCTTCTACAAAGCTGATCACTCAATCTCT 948
QY 1021 CTATATGATCTTACAAAGACCTGTTGAAAGCTTAAACACTTCAATCTCTAGCTG 1080
DB 949 CTATATGATCTTACAAAGACCTGTTGAAAGCTTAAACACTTCAATCTCTAGCTG 1008
QY 1081 GAAAGATAGAGATTCCTCAATATATAACACAGATGTTTCAACCTCAAGAAATCTTCT 1140
DB 1009 GAAAGATAGAGATTCCTCAATATATAACACAGATGTTTCAACCTCAAGAAATCTTCT 1068
QY 1141 CACAT 1145
DB 1069 CACAT 1073

RESULT 14
US-09-928-175-22
; Sequence 22, Application US/09928175
; Patent No. US20020123618A1
; GENERAL INFORMATION:
; APPLICANT: Parzly, Christopher J.
; APPLICANT: Gong, Jianhua
; APPLICANT: Daugherty, Betsy
; APPLICANT: Rogers, No. US20020123618A1
; TITLE OF INVENTION: Leucine-Rich G Protein Coupled Receptor-8 Molecules and
; FILE REFERENCE: 00-1229
; CURRENT APPLICATION NUMBER: US/09/928.175
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/224,455
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 1140
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1140)
US-09-928-175-22

Query Match 36.5%; Score 825.8; DB 10; Length 1140;
Best Local Similarity 83.1%; Pred. No. 4e-207;
Matches 941; Conservative 0; Mismatches 192; Indels 0; Gaps 0;

QY 113 GTAGCATGATCATCTCTTCAATGCAAAAGATATTTTCTGGAATCTTACCAAGT 172
DB 5 GCAGTATGAGGCTCTCTGCTGCCCCCAAGGATATTTTCTGGAATCTTACCAAT 64
QY 173 GCTTACCCCGAGCTTTTCACTGTGATGCAAGATGACTGTGGGACGCGGCGAGAG 232
DB 65 GCTTACCCCGAGCTTTTCACTGTGATGCAAGATGACTGTGGGACGCGGCGAGAG 124
QY 233 AGAACTGTGTGACACTAGTGTGATGGCGACCATATTTTGGCAACAGTCAATGCTTA 292
DB 125 ACAACTGTGTGACACTAGTGTGATGGCGACCATATTTTGGCAACAGTCAATGCTTA 184
QY 293 ACAAGCGGCTTAAACAGAGAGCTTCTTAAACAGTATTCACATGCTGTGAGCTGCA 352
DB 185 ATAAAGGACATGACACAGAGAGCTTCTTAAACAGTATTCACATGCTGTGAGCTGCA 244
QY 353 AAGAACTGAATGGAATGTGTAAATGTGACTTAAAGCTGTGCGGATATTTCTTACA 412
DB 245 GAGAAATGGAATGTGTAAATGTGACTTAAAGCTGTGCGGATATTTCTTACA 304
QY 413 ATGTGACATTAATCTCTCTTAAAGAAACAAATTCACAGCTTCCAGATTAAGTTTCA 472

DB 305 AGTAACTATTAATCTCTTAAAGAAACAAATTCACAGACTTCAAGTCTTCA 364
QY 473 TCAAAATACACAAACTTAAAGATATTTTCTTACAGATTAATGCAATGACATATCCA 532
DB 365 GCAGATACACAGAACTCAAGAAATATCTTACACAGACTTCAAGTCTTCAAGTCTTCA 424
QY 533 GGAAGCAATTTTGGATTAATGATCTGCAAAATATTAATGATCTCAACCAATGATCA 592
DB 425 GGAGAGCAATCTTGGATTAATGATCTGCAAAATATTAATGATCTCAACCAATGATCA 484
QY 593 CAACCTCAGACCTGGAATATTTCAAGAGCTTACATCAGCTTAACTTGGATTAATG 652
DB 485 CTTCTCAGAGCTGCTGGAATATTTCAAGAGCTTACATCAGCTTAACTTGGATTAATG 544
QY 653 ACAATTCATTAACAGAAATTTTCAAGAGCTTAACTTGGATTAATGATTAATCTTCTTCC 712
DB 545 ACAACCCGATCACAGAAATCTCAAGAAATCTTAAATGAGGATTAATCTTCTTCTTCT 604
QY 713 TGTCTATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 772
DB 605 TGTCTATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 664
QY 773 AACTCAACTGAGTGAATTTGAAAGCAATGAAATGATCTCAAAATCTTACGTTTC 832
DB 665 AACTCAACTGAGTGAATTTGAAAGCAATGAAATGATCTCAAAATCTTACGTTTC 724
QY 833 TGTCTGATGATCTGCTCAAGCTGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 892
DB 725 TAAAGTGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 784
QY 893 AGAAGCAATTTTCTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 952
DB 785 AGAAGCAATTTTCTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 844
QY 953 CGAGCTATGACCTTCACTTTTAAAGACTGAACTTCAAAAGCTGAACTGCTCAT 1012
DB 845 CAAACCTCCAGTCACTTCTTCAAGCACTTCACTTCTTCAAGCACTTCAAGCACTTCTCAT 904
QY 1013 CCAATCTCTTATGATCTTCAAGCACTTCAAGCACTTCAAGCACTTCAAGCACTTCTCAT 1072
DB 905 CCAATCTCTTATGATCTTCAAGCACTTCAAGCACTTCAAGCACTTCAAGCACTTCTCAT 964
QY 1073 TAGACCTGAAAGATGAGATTTTCAAAATATTAACAGAAATGTTTCAACCATGAGAA 1132
DB 965 TAGACCTGAAAGATGAGATTTTCAAAATATTAACAGAAATGTTTCAACCATGAGAA 1024
QY 1133 ATCTTCTCAATTTATTTCAAAACTTTGCAATGCTGCTGCTGCTGCTGCTGCTGCT 1192
DB 1025 ACTTCTTCAATTTATTTGAAACCTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1084
QY 1193 TATGATGCTTGAAGCAAGCACTTCTTCAATGAGCACTTGGCTTAAC 1245
DB 1085 TCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1137

RESULT 15
US-10-225-567A-622
; Sequence 622, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: Lifespan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTOR
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 622
; LENGTH: 2274
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-225-567A-622

Query Match 32.5%; Score 735; DB 14; Length 2274;
Best Local Similarity 60.9%; Pred. No. 5,9e-183;
Matches 1263; Conservative 0; Mismatches 785; Indels 27; Gaps 3;

QY 112 GGAATTTTCCCTGGGAAATCTTACCAAGTCTTACCCGAGCTTTCACTGTATGCG 201
DB 88 GGCATTTCCCTGGGAAATCTTACCAAGTCTTACCCGAGCTTTCACTGTATGCG 147
QY 202 AAGATGACTGTGGAAACGGGCGGACGAAGAACTGTGTGACACTAGTGGAGG 261
DB 148 GTGAGACAGCTGGGAAATAGGCCCACTGTGAGACACACATGATGCTC 207
QY 262 ACCATATTTGGACAGTGCATGGAATGCTAAC-----GCGTG 300
DB 208 ATGCAATTTGACAAATATATTTGGCAGTTACTACAAATAGACTCCCAATATCTTTAG 267
QY 301 GCTTAAACAGAGAGCTTTCTTAAACAGTATCCCAATGCTGTACTGCAAGAACT 360
DB 268 GAGAAACACCTGAATGTTGGTGGTCTGTGCGCAGTCAATGTCTTTGCAAGGCTG 327
QY 361 GAATTTGAATGTAAATGTGACTTAAAGTCTGTGCGGATGATTTCTAACAATGACA 420
DB 328 GAGCTTGACTGTGATGAAACCAATTTACAGAGCTTTCCATCGGTTTCTCAATGTGACT 387
QY 421 TTACTGTCTTTAAGAAAAACAATTCACAGTCTTCAAGATTAAGTTTCAATCAATAC 480
DB 388 GCAATGTCACTTCAAGTGAATTAATTAAGAAAGCTTCTCGATTTGCTTCAAGATTAAT 447
QY 481 ACAAACCTTAAAGATTTCTTCCAGCAATTTGATGATGACACATATCCAGAAAGA 540
DB 448 CATGATCTTCAAGAGCTGTAACCTGCAAAACAATTAATTAATCACTTCAATGT 507
QY 541 TTTTGTGATTAATGATCTGCAATATTAATCTCAACACAACTGCATCAACCTTC 600
DB 508 TTCAAGAGACTGAATAGCTTAACTGATTAATCTGATCAATTAAGAAATACCTTCG 567
QY 601 AAGCTGGAATATTTCAAAGACTTACAGCTAATCTTGGCTAATTTAATGACAAATCA 660
DB 568 AAGCCGGGTGTTTGAAGATCTTCAAGACTAAGTGTGATTAATGAAGTAAATCA 627
QY 661 ATTAACAGAAATTTCAAGGCTTTGTTACGGGATTAATTCCTGTTTCCGCTAG 720
DB 628 CTCAGTGAATTTCCCAACACATTTATGACTTAATTTCTTATCTTATGCTG 687
QY 721 GTTAATTAATTAATTAAGTCTTCC---CAAGCAGATGTGCCCCAAATGCTCAATC 777
DB 688 ATGAATTAAGTCTTCAACCGGTTTAACTGATTAATCTCTGCAACATGCCAATCA 747
QY 778 AACTGGGTGATTTGGAAGCAATGAATTAATTAATCTCAAAATTTCAAGTTTCTG 837
DB 748 CATTTGCTGACCTTGAAGCAACATTAATTAATTAAGAAATTTGACTTTATTTCC 807
QY 838 TGGATTTGCTCAAGTGTGTTCTGCTAGAAATCAAATGGTTTGTTCAGAGAG 897
DB 808 TGCAGTAATTAATCTGTTTATGATGAGAAACAAATTAATCACTTAATGAAT 867
QY 898 ACATTTTCTTCAATTAATAATTAAGAGAACTGATCTGTCTAGCAATAGATAGCGAG 957
DB 868 ACTTTTGAACCTCTCCAGAAATGATGATTTGAGAGTAATTAAGATTAAGAAAT 927
QY 958 CTATCACTTCACTTTTAAAGCTTGAAGCTTCAAAAGCTGAACCTGTATCAAT 1017
DB 928 CTTCACCGCTTAATTAATTAAGAGCTGAAGAGCTGTCAATTTGATCTTCTTAAT 987
QY 1018 CCTCTATGATCTTCAAGAAACAGTTGAAGCTTAAACAATTTCAAGTCTAGAC 1077
DB 988 CCAATCCAAATTAATTAAGCAACCAATTTGATTAATCTTGTCAAACTCAAGTCTCAGC 1047

QY 1078 CTGAAAGATAGATTCATAATATAACACAGAAATGTTCAACCCATGAAATCTT 1137
DB 1048 CTAGAAGAGATTGAATTTCAATATCCAAACAAAGAAATGTTAAGCTTATGATCTC 1107
QY 1138 TCTCATTTTTCATAAAATCTTGCATCTGCTCTATAGCTCCCATGTCGAATAGT 1197
DB 1108 TCTCATATATTTTAAAGAAATTCAGATCTGTGGATGACCAACATGTTGCGAGCTGT 1167
QY 1198 ATGCCCTTACAGGACCGGACTTCTCATTTAGAGACCTCTGGGCTAACATATCTCAGA 1257
DB 1168 AAACCAACACTGATGAAATTTCACTTGAAGATCTTGTGGACAGATTTTACAGAA 1227
QY 1258 ATATTTGTCTGGTTATAGCTTTCAATACCTGTCTTGGAAATCTTTTGTCAATGGCATG 1317
DB 1228 GTATTTGTCTGGTTATAGCTTTCAAGTTACCTGCTTTGAAACATTTTGTCAATGGCATG 1287
QY 1318 AGATTTTCAATTAAGCTGAATAATCAACCTGATGTCATTAATAATCTTTGTTGT 1377
DB 1288 CGACCTTATATCAGGCTGAGAACACAGCTGTATGCTCATATCTTCTCTGCTGT 1347
QY 1378 GCTGATGCTGATGAGGTTTACTGTCTTGTGTCATTTTGTATTAATAATACGA 1437
DB 1348 GCGACTCTTATAGGAAATATTTATTCGATGAGAGCTTTGACCTTAAGTTGCT 1407
QY 1438 GGGCAGTATCAGAAATATGCTTGTGTGATGAGACGTGCACTGCGGCTCATGGG 1497
DB 1408 GGAGAAATCAATTAAGCATGCGGAGCTGTGATGAGAGATCACTATGTCACTGTAGGA 1467
QY 1498 TTCTGGGCAATGCTGTCCACCGAAGTCTGTCTGTCTAGTCACTTCACTTGGAG 1557
DB 1468 TCTTTGGGCAATGCTGTCCACAGAAATATCAGTTTATCTGTAACTTTCTGACATTTGAA 1527
QY 1558 AAGTCTGTGATGCTTCTCCCTCAGTAACTTGCACCTGGAAGAAACGAGACCTCA 1617
DB 1528 AATATCATCTGATTTGTATCTTTTGAATGTGAACTCGAAATATGCAAAAT 1587
QY 1618 GTATCTCATTTGATCTGATGAGGAGATTTTAAATAGCTAATTCATTTGGAT 1677
DB 1588 ACAGTTTGAATCTCATTTGATGATCTGTTTATAGGCTTTCATTTCAATTTGAGCAT 1647
QY 1678 AAGATTAATTTGGAACCTTTTAAAGGAAATGAGATGTTTCCACTTATATGAC 1737
DB 1648 AAGGAATTTTCAAAACATCAATGACACCAATGAGATGCTTCTCTTCAATTCAGAA 1707
QY 1738 CAACAGAAATATTTGAAGCAAGGATATCTCTTGAATTTTCTAGGTGCACTTG 1797
DB 1708 GATACAGAAATTTGAGGCCAGATTTATTCAGTGCATTTTCTTGATTTAATTTG 1767
QY 1798 CTGGCTTTTCTGATGATGTTGTTTCTTAATTAATTAATGTTCTGTTCAATCAAAAACC 1857
DB 1768 GCCGATTAATCATATGATTTTTCATAGGAACATGTTTATAGTTCATCAAAAGT 1827
QY 1858 GCTTGCAGACCAAGAAATGAAATGTTTGAAGAGAGTGTGCTTCCAAATGCT 1917
DB 1828 GCCATTAACGAACTGAATTAAGAAATCAAGTAAATAAAGAAATATCTTCCAAACGT 1887
QY 1918 TTTCTTTTATAGTGTCTGTATGCAATCTGATCTGATCTTCTGATTTGATTAATTC 1977
DB 1888 TTTTCTTTATAGTATTTATGATGATTTATGATGATTTTGTGATGATTAATTT 1947
QY 1978 CTTCCTCTCTTCCGGGTGAAATACCAACATATGCTCTGATATGATTTTTC 2037
DB 1948 CTTCATCTGCTTCAAGTGAATTAACAGATACCAATCTCTGTGGATGATTTTAT 2007
QY 2038 CTTCAGTTAAAGAGCTTTGAATCCATCTCTTAATCTTCAACCAACTTTTATAG 2097
DB 2008 CTGCCATTAACAGTCTTTGAACCAATCTCTTAATCTTCAACCAAGACATTTTAA 2067
QY 2098 GACAAGTTGAACACCTGCTGCAAAAC---TCAGAGAAATCAATTTTCAAAATTA 2154
DB 2068 GAAATGATTCATGCTTTTGTATTAATTAACAAAGAAATCTATGAGCAAGAGT 2127

QY 2155 AAAAAAGTTATCTACATCCATTGTTGGATAGA 2189
| | | | | | | | | | | | | | | | | |
Db 2128 CAGAAACATATGCTCCATCATTCATCTGGTGA 2162
| | | | | | | | | | | | | | | | | |

Search completed: November 28, 2003, 19:32:11
Job time : 732 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 28, 2003, 15:41:35 ; Search time 4260 Seconds

(without alignments)
12922.450 Million cell updates/sec

Title: US-09-928-175-1

Perfect score: 2265
Sequence: 1 atgattgtttcttcggtttt.....taatgaaccagtttcttag 2265

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 22781392 segs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

EST:
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estcov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_esthum:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_pro:*
26: em_gss_phg:*
27: em_gss_vrt:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1249.8	55.2	2386	11 AK034592	AK034592 Mus muscu
2	466.8	20.6	2838	11 AK047861	AK047861 Mus muscu
3	383.2	16.9	609	9 AV592706	AV592706 AV592706
4	378	16.7	648	10 BB62659	BB62659 BB62659

5	306.2	13.5	758	13 BX084029	BX084029 BX084029
6	296.2	13.1	841	13 BQ228832	BQ228832 AGENCOURT
7	290.2	12.8	648	14 CB216867	CB216867 NISC ng09
8	288.8	12.8	461	9 AV592705	AV592705 AV592705
9	257.4	11.4	300	9 AM307854	AM307854 1346 MARC
10	228.8	10.1	549	28 AQ394779	AQ394779 CITRBT-EL-
11	224.6	9.9	279	10 BF040869	BF040869 BP250001A
12	190.6	8.4	857	13 BU366143	BU366143 603585541
13	190.4	8.4	739	29 BX178051	BX178051 Danto rer
14	190.4	8.4	777	29 BX146122	BX146122 Danto rer
15	188.6	8.3	532	28 AZ319928	AZ319928 IM0039D13
16	186.2	8.2	197	10 BF942735	BF942735 EST-CD15N
17	186.2	8.2	197	12 BM280297	BM280297 3'EST-NCN
18	184.6	8.2	235	9 AM436170	AM436170 75600 MAR
19	183.2	8.1	631	9 AL955885	AL955885 AL955885
20	183	8.1	408	28 AQ212353	AQ212353 HS_3002_B
21	181.6	8.0	811	13 BU366385	BU366385 603786975
22	179	7.9	456	10 BF021857	BF021857 UY56H08.Y
23	177.4	7.8	574	10 BB632910	BB632910 BB632910
24	177.4	7.8	1307	11 AK039086	AK039086 Mus muscu
25	174.8	7.7	1472	11 AK054129	AK054129 Mus muscu
26	171.2	7.6	744	10 BG304121	BG304121 F130F05.X
27	168.6	7.4	635	13 BQ078630	BQ078630 f479b08.Y
28	164.4	7.3	873	13 BU274328	BU274328 603532573
29	161.8	7.1	198	14 CA97681	CA97681 EST_LGR8
30	161.6	7.1	661	13 BU274919	BU274919 603531625
31	154.4	6.8	516	10 BF158267	BF158267 F130F05.Y
32	149.6	6.6	628	10 BB665906	BB665906 BB665906
33	145.8	6.4	307	12 BM955900	BM955900 EST0837.H
34	144.2	6.4	627	12 BM425549	BM425549 p9f2c.pk0
35	129.6	5.7	1884	11 AK045269	AK045269 Mus muscu
36	128	5.7	720	14 CD218149	CD218149 p9f1n.pk0
37	124	5.5	786	28 AQ745959	AQ745959 HS_2275_A
38	121.8	5.4	527	10 BB648375	BB648375 BB648375
39	118.8	5.2	593	28 AQ053279	AQ053279 CTR-HSP-2
40	116.8	5.2	644	28 AQ059136	AQ059136 HS_5424_B
41	106.4	4.7	696	29 BX158268	BX158268 Danto rer
42	106	4.7	513	28 AQ059313	AQ059313 HS_5335_B
43	104.8	4.6	686	13 BU284397	BU284397 603865563
44	101.4	4.5	1078	29 CC244249	CC244249 CH261-120
45	95.8	4.2	702	10 BB297224	BB297224 BB297224

ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	MEDLINE
AK034592	AK034592	Mus musculus 12 days embryo embryonic body between diaphragm region and neck CDNA, RIKEN full-length enriched library, clone:9430012D19 product: similar to G PROTEIN COUPLED RECEPTOR AFFECTING TESTICULAR DESCENT, full insert sequence.	AK034592	AK034592.1	GI:26330052	HTC; CAP trapper.	Mus musculus (house mouse)	1	Carninci, P. and Hayashizaki, Y.	High-efficiency full-length cDNA cloning	JOURNAL	20499374
AK034592	AK034592	Mus musculus 12 days embryo embryonic body between diaphragm region and neck CDNA, RIKEN full-length enriched library, clone:9430012D19 product: similar to G PROTEIN COUPLED RECEPTOR AFFECTING TESTICULAR DESCENT, full insert sequence.	AK034592	AK034592.1	GI:26330052	HTC; CAP trapper.	Mus musculus (house mouse)	2	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes	JOURNAL	20499374
AK034592	AK034592	Mus musculus 12 days embryo embryonic body between diaphragm region and neck CDNA, RIKEN full-length enriched library, clone:9430012D19 product: similar to G PROTEIN COUPLED RECEPTOR AFFECTING TESTICULAR DESCENT, full insert sequence.	AK034592	AK034592.1	GI:26330052	HTC; CAP trapper.	Mus musculus (house mouse)	3	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes	JOURNAL	20499374
AK034592	AK034592	Mus musculus 12 days embryo embryonic body between diaphragm region and neck CDNA, RIKEN full-length enriched library, clone:9430012D19 product: similar to G PROTEIN COUPLED RECEPTOR AFFECTING TESTICULAR DESCENT, full insert sequence.	AK034592	AK034592.1	GI:26330052	HTC; CAP trapper.	Mus musculus (house mouse)	4	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes	JOURNAL	20499374

REFERENCE AUTHORS	PUBMED 11042159
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Komuro, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, Y., Ohara, E., Wachihi, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.	
TITLE	RIKEN integrated sequence analysis (RISA) system -384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE	20530913
PUBMED	11076861
REFERENCE AUTHORS	4
Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Aizawa, T., Hara, A., Fukunishi, Y., Komuro, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamana, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Plechmann, W., Gaasterland, T., Giesi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaide, I., Pesole, G., Quackenbush, J., Schiraldi, L.M., Staudt, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Balderelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carinci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Guernicich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombae, P., Nordone, P., Ring, B., Ringwald, C., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyooka, K., Wang, K.H., Weitz, C., Whitaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawai, H., Kohseuti, S. and Hayashizaki, Y.	
TITLE	Functional annotation of a full-length mouse cDNA collection
JOURNAL	Nature 409 (6821), 685-690 (2001)
MEDLINE	21085660
PUBMED	11217851
REFERENCE AUTHORS	5
The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.	
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL	Nature 420, 563-573 (2002)
MEDLINE	6 (bases 1 to 2366)
PUBMED	1217851
REFERENCE AUTHORS	6
Adachi, J., Aizawa, K., Akimura, T., Aizawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, M., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Komuro, H., Konda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, Y., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takeuchi, A., Tanaka, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.	
TITLE	Direct Submission
JOURNAL	Submitted (16-JUL-2001) Yoshihide Hayashizaki. The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
COMMENT	CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL: http://genome.gsc.riken.go.jp/ URL: http://fantom.gsc.riken.go.jp/.

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	Matches 1440; Conservative 0; Mismatches 317; Indels 0; Gaps 0;	
QY	32	TCAGCCTCAGATTGATTAACATGTTCTTCTACCTCATTCATTCGTTGATCATGCA 91
DB	87	TCAGCGCACACCGGCGCAATGTGGCTCTCTCATCATCATCTTCTGACGAGGTCA 146
QY	92	AAAGTTTTCATCTGACTCAAGTAGATGATCACTCTCTTCAAGCCAAAAGATATTTC 151
DB	147	AAAGTTTTCATCTGCTGACACAGATGATGCTCTCTGTCGCCAAAAGGATATTTC 206
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DB	207	CTGTGGGAATCTTACCAAGTCTTACCCGAGCTTTTCACTGTGATGCAAGATGACT 266
QY	212	GTCGGGAACGGGCGGCGAAGAACTGTGTGACACTGTGTGATGGGACCATATTTC 271
DB	267	GCGGGGAATGTGTGCGGCGAAGAACTGTGTGACACTGTGTGATGGGACCATATTTC 326
QY	272	GCAAGATGATGGAATGCTAAGCGGTGCTTAAACAGAGAGTCTTAAACAGT 331
DB	327	GCAAGATGATGGAATGCTAAGCGGTGCTTAAACAGAGAGTCTTAAACAGT 386
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QY	392	CTGTGCGCATGATTTTAAACATGTGACATTAAGTCTTAAAGAAACAAATTCACA 451
DB	447	CTGTGCGCATGATTTTAAACATGTGACATTAAGTCTTAAAGAAACAAATTCACA 506
QY	452	GTCCTCAGATTAAGTTTCAATCAATACCAAAATTAAGATATTCTTCAGACATA 511
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Oy	812	ATCTCACAAAATTTACAGTTTCGTGCTGAGAGTGGCTCACAGTGGTGTTCGCTCAAA	871
Db	867	ACATPAACACATCCACCTTCTCTAACGTGTGACTGCTCAACGGTGTGTTCTGCTCAAA	926
Oy	872	ATCAAAATGTGTTGTTGTTCCAGAGAGACATTTCTTCATTAATAAAATTTAGAGAACATCG	931
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Oy	932	ATCTGTCTAGCAATACGATTAACGGAGCTATCACCTCACCTTTTAAAGACTTCAACCTTC	991
Db	987	ACCTGTCTAGCAAAATTAAGATTAACAAACCTCCAGTCCACCTTTTCCAGCACCTTCACTTC	1046
Oy	992	TACAAAACCTGAACCTGTCAATCAATCTCTATATCTTACACAAGAACAGTTTGAA	1051
Db	1047	TCGAGAACTGAACCTGTCAATCAACCTCTCTGTATATGTCCACAAGAACAGTTTGAA	1106
Oy	1052	GTCTTAAACAACTTCAGTCTCTAGACCTGGAAAGATAGAGATTCGAATATTAACACAC	1111
Db	1107	GTCTCAAAACAATTCAGTCTCTAGACCTGGAAAGATAGAGATTCGAATATTAACACAC	1166
Oy	1112	GAAATGTTCAACCCAGTGAAGAAATCTTTCACATTTATTTCAAAAACCTTGGATACCTGT	1171
Db	1167	GAAATGTTCAACCCAGTGAAGAAACCTTTCACATTTATTTGAAAAACCTTGGATACCTGT	1226
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Db	1227	CCTATGCTCCCATGTCGGAATCTGATATGCCGCTGACATGATGATATTTCTTGTGTGAAG	1286
Oy	1232	ACCTCTTGGCTPAACAATATCTCTCAGAAATTTGTCTGGGTTATAGCTTTCAATTAACCTGT	1291
Db	1287	ACCTCTTGGCTPAACGATATCTCTCAGAGATCTGTCTGGGTTATTAACCTTTCATTAACCTGT	1346
Oy	1292	TTGGAATATCTTTTGTGATTTGGCATAGAGATCTTTCAATTAAGCTGAAATTAACAATCAGC	1351
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Oy	1412	TTGGCAATTTTGGATATPAATAATPAACGAGGCAATATACAGAAAGTATCCCTTGGTGGATAGG	1471
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Oy	1472	AGAGCGTGAAGTGCAGCTCATGGGATTTCTGGCAATGCTGTCAACGAAAGTCTCTGTGTT	1531
Db	1527	AGAGGTGTGCTGCGCGCTGCTGGGCTTCTGGCAACGCTGTCAACAGAGTCTCTGGTGG	1586
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Db	1587	TGCTGTGACATTTCTGACGCTGGAGAAATTTCTTGTCAATATATTTCCCTTTCACAAAC	1646

Qy	1592	TTGACCTGGAAAAAGGAGACCTCAAGTCATCCATCTTGACATCTGATGGCCGGAATTT	1651
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Qy	1652	TAAATAGCTGTATATTCATTTTGGATTAAGGATTATTTTGGAACTTTTATGGGAAAAATG	1711
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LOCUS	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
AK047861	AK047861	1	GI:26339011	HTC, CAP trapper.	Mus musculus (house mouse)
DEFINITION	Mus musculus 16 days embryo head cDNA, RIKEN full-length enriched library, clone:c130013110 product:similar to G PROTEIN COUPLED RECEPTOR AFFECTING TESTICULAR DESCENT, full insert sequence.				
REFERENCE	Carninci, P. and Hayashizaki, Y.	1	High-efficiency long-length cDNA cloning		
AUTHORS	TITLE				
JOURNAL	Mechn. Enzymol.	303,	19-44 (1999)		
MEDLINE	99279253				
PUBMED	10349636				
REFERENCE	2				
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.				
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes				
JOURNAL	Genome Res.	10 (10),	1617-1630 (2000)		
MEDLINE	20499374				
PUBMED	11042159				
REFERENCE	3				
AUTHORS	Kono, H., Akizawa, J., Nishikawa, K., Kitagawa, S., Sasakura, N., Carninci, P., Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kasaiyagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Itawa, M., Ohara, E., Watanabe, K., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunaga, S., Kawaji, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A., and Hayashizaki, Y.				
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multiplexed sequencer				
JOURNAL	Genome Res.	10 (11),	1757-1771 (2000)		
MEDLINE	20530913				
PUBMED	11076861				
REFERENCE	4				
AUTHORS	Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Akizawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, U., Fukuda, S., Aizawa, K., Irawa, M., Nishikawa, K., Kiyosawa, H., Kondou, S., Yamanka, I., Salto, T., Okazaki, Y., Gojobori, T., Bono, H., Kanakawa, T., Salto, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, A., Flatschman, W., Gaasterland, T., Gissi, C., King, B., Kochiya, H., Kuschi, P., Lewis, S., Matsuo, Y., Nukado, I., Pesole, G., Quackenbush, D., Schmitt, L.M., Staudt, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barab, G., Blake, J., Boftelli, D., Boljuna, N., Carninci, P., de Bonaldo, M.P., Brownstein, M.J., But, C., Fletcher, C., Fujita, M., Gaibaldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D.A., Kamuya, M., Lee, N.H., Lyons, P., Machinomi, L., Mashima, J., Mazzarelli, J., Mommaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H.,				

Sato, K., Schonbach, C., Seta, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyono, K., Wang, K.H., Weitz, C., Whitaker, C., Wilming, L., Wyshak-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kontseki, S. and Hayashizaki, Y.

TITLE
Functional annotation of a full-length mouse cDNA collection

JOURNAL
Nature 409 (6821), 685-690 (2001)

MEDLINE
21085660

PUBMED
11217851

REFERENCE
5

AUTHORS
The PANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL
Nature 420, 563-573 (2002)

REFERENCE
6 (bases 1 to 2838)

AUTHORS
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T., Horii, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawaji, H., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

TITLE
Direct Submision

JOURNAL
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

FEATURES
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1. 2838
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Matches 534; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

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DB 348 CAGTATTTGAAAACCTTCGATGCTGCTCTATGCTCCCATGTCGGAATATGATGCC 407

QY 1203 CTTCGAGGAGGAGGATTTCTTCATTTGAGAGCTCTTGAGCTAAATATCTCAGAAAT 1262
DB 408 GTGAGCTAGTATGATTTCTTGCTGAGAGACCTTGAGCTAAATATCTCAGAGTGTG 467

QY 1263 TGTCTGGATTATGCTTCATTTCAATTCCTGCTGGAATCTTTTGTTCATGGATGATC 1322
DB 468 TGTCTGGATTATGCTTCATTTCAATTCCTGCTGGAATCTTTTGTTCATGGATGATC 527

QY 1323 TTTCTATTAAGCTGAAAATACATCAGCTATGTCATCAAAATCTTTGTTGCTGTA 1382
DB 528 TCTCATTAAGCTGGAATACAACTCAGCTATGTCATCAAAATCTTTGTTGCTGTA 587

QY 1383 TTGCTGATGGGTTTCTTCTTCTTGTGGCATTTTCATTAATAACGAGGGA 1442
DB 588 TTGCTGATGGGTTTCTTCTTCTTGTGGCATTTTCATTAATAACGAGGGA 647

QY 1443 GTATCAGAAAGTATGCTGCTGCTGATGAGAGCGTCAGTCCGCTCAGGGTCTCT 1502
DB 648 GTATCAGAAAGTATGCTGCTGCTGATGAGAGCGTCAGTCCGCTCAGGGTCTCT 707

QY 1503 GGCATGCTGTCTCCAGCAAGTCTCTGTTCTGTATGACCTTGAATTTGAGAAAGTT 1562
DB 708 GGCATGCTGTCTCCAGCAAGTCTCTGTTCTGTATGACCTTGAATTTGAGAAAGTT 767

QY 1563 CTTGCTGATTTCTTCCCTTCTGATGATGAGAGCGTCAGTCCGCTCAGGGTCTCT 1622
DB 768 CTTGCTGATTTCTTCCCTTCTGATGATGAGAGCGTCAGTCCGCTCAGGGTCTCT 827

QY 1623 CCTCATTTGATCTGAGAGCGGATTTTAAATGCTGTAATTCATTTGGAATAGGA 1682
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QY 1683 TTATTTGGAATCTTTATGAGGAAAATGAGATGTTCCGACTTATGAGCAAC 1742
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QY 1743 AGAAGATTTGGAAGCAAGGATTTCTTGGAAATTTTCTTAGGT 1788
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RESULT 3
AV592706 609 bp mRNA linear EST 27-NOV-2001
LOCUS AV592706 Bos taurus cartilage fetus Bos taurus cDNA clone
DEFINITION E1CA032808 5', mRNA sequence.
ACCESSION AV592706
VERSION AV592706.1 GI:9707863
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.
1 (bases 1 to 609)
Takaue, A., Hirotsune, S., Itoh, R., Itohono, A., Suzuki, H., Aso, H. and Sugimoto, Y.
Establishment of a high throughput EST sequencing system using poly(A) tail-removed cDNA libraries and determination of 36,000 bovine ESTs
Nucleic Acids Res. 29 (22), E108 (2001)
JOURNAL MEDLINE 21570554
PUBMED 11713328
CONTACT: Yoshikazu Sugimoto
Animal Genetics Division

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Odakura, Mishigino, Nishitani-shirakawa, Fukushima 961-8061, Japan
Tel.: 81-248-25-5641
Fax: 81-248-25-5725
Email: kazunugi@cocoa.com.ne.jp

Single-pass sequencing.
This clone was obtained from a polyA-deleted cDNA library.

FEATURES

Source

BASE COUNT	ORIGIN
128 a	137 c 145 g 189 t 10 others

Query Match	16.98;	Score 383.2;	DB 9;	Length 609;
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Oy	1188	CCGAATATGTAATGACCTTGGACGAGCGGATTT--CTTATTTGAGG--ACGCTGGGCTA	1244
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Oy	1476	CGTGAATGCGGCTCTCATGGGGTTCCTGGCCATGCTGTCCACCGAAATCTCTGTCTGCT	1533
Dp	312	CTTGAAGTGGCGGCTCTCGGGCTTCTTGCCATGCTGTCCATGAGGTCTCTGTCTCTT	371
Oy	1536	ACTGACCTACTGACTTTGGAGAAATGTCCTGATATGTCCTCCCTCAGTAACATTCG	1599
Dp	372	GCTCACAATCTTGACCTCGAGAAATTCCTGGCGGTGTCTTCCCTTCAGTAACATTCG	431
Oy	1596	ACCTGAAAAACGGCAGACCTCAGTATCTCATTTTGCATCTTGATGAGCGGAAATTTTAT	1655
Dp	432	TCTGGAAAAATGGCAGACCTCGCGCTCTATCTGCATCTGGAATGAGGGTCTTAT	491
Oy	1656	AGCTGTAAATTCATTTTGGAAATAGGAATTTATTTGGAAAATTTTATGAGAAAAATGAGT	1715
Dp	492	AGCTGGGACTCATATGNGAAAAAGAGATTTATTTGGAAAATTTTATGAAAAAATGAGT	551
Oy	1716	ATGTTTCCCACTTATTTATGACCAACAGAAATATGGAAGCAAAAGGTATCTCTT	1773
Dp	552	ATGTTTCCCACTTATTTATGACCAACAGAAATATGGAAGCAAAAGGTATCTCTT	609

RESULT 4					
BB626659					
LOCUS					
DEFINITION	BB626659	648 bp	mRNA	linear	EST 26-OCT-2001
	BB626659 RIKEN full-length enriched, 12 days embryo, embryonic body,				
	between diaphragm region and neck Mus musculus cDNA clone				
	9430012D19 5', mRNA sequence.				

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BB626659
BB626659.1 GI:16464583
EST.
Mus musculus (house mouse)
Mus musculus

TITLE
JOURNAL
COMMENT

Laboratory of Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suenohiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan
Tel.: 81-45-503-9222
Fax: 81-45-503-9216

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. *Genome Res.* 10 (10), 1611-1630 (2000)

wagci, K., Fujiyama, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanishi, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunaga, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A. and Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. *Genome Res.* 10 (11), 1757-1771 (2000)

Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. *Genome Res.* 11 (2), 281-289 (2001)

Kondo, S., Shingawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Hayashizaki, Y.

Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. *Mamm. Genome* 12, 673-677 (2001)

Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

e mouse tissues.

FEATURES

Bouyce

```

location/Qualifiers
1.648
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="9430012D19"
/issue_type="embryonic body between diaphragm region and
neck"
/dev_stage="12 days embryo"
/lab_host="DH10B"
/clone_1bp="RIKEN full-length enriched, 12 days embryo,
embryonic body between diaphragm region and neck"
/note="Site 1: SalI; Site 2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN, Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5',
GAGAGAGAGAGATCCAGAGCTCTTTTTTTTTTTTTNN 3'], cDNA was
prepared by using triethanol thermo-activated reverse
transcriptase and subsequently enriched for full-length b

```

cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 370.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAAATTAAATTCCTCCCTCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI."

BASE COUNT 191 a 164 c 137 g 156 t

Query Match 16.7%; Score 378; DB 10; Length 648;

Best Local Similarity 79.5%; Pred. No. 1.9e-69;

Matches 447; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

32 TCAGCCTCAGATTGATTACAGTCTTTCTTACTTATTCATCTGTTGATGATGCA 91
 87 TGGAGGCGACACCGCGCGAGTGTGCTCTTATTCATGTCATCTTCTGACGAGGTCA 146
 92 AAGATTTTGACTGACTCAAGGTAGATGATCACTCTCTTCAGCCCAAAAGATATTTTC 151
 147 AAGATTTTGACTGCTGACGAGATGATGCTCTCTCTGTCCTCCCAAGGGTATTTTC 206
 152 CCGTGGGATCTTACCAAGTCTTACCCGACCTTTTCACTGATGAGCAAGATGACT 211
 207 CCGTGGGATCTTACCAAGTCTTACCCGACCTTTTCACTGATGAGTGTGATGAT 266
 212 GTGGGAACGGGCGGCGAGAGAGACTGTGTGATCACTAGTGGATGGCGACATATTTG 271
 267 GCGGAGATGCTGCGAGAGAGACACTGTGTGATCACTAGTGGATGGAGACATATTTG 326
 272 GCACAGTGCATGGAATGCTTAACAGCGTGGCTTTAAACAGAGTGGCTTTTAAACAGT 331
 327 GCACAGTGCATGGAATGCTTAACAGCGTGGCTTTTAAACAGAGTGGCTTTTAAACAGT 386
 332 ATCCACAAATGCTGATCTGCAAGAGAACTGAATTTGATGTAATGGAATGGAATGGAAT 391
 387 ATCCACAAATGCTGATCTGCAAGAGAACTGAATTTGATGTAATGGAATGGAATGGAAT 446
 392 CTGTGCGATGATTTCTTAACATGTGACATTAATGCTGCTTTAAAGAAAACAAATTCACA 451
 447 CTGTGCGAAGGTTTCATCAACATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 506
 452 GTCTTCCAGTAAGTTTTCATCAACATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 511
 507 GACTTCCAGTAAGTTTTCATCAACATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 566
 512 ATTCATTAGACATATTCAGAGAAAGCATTTTGGATTATGTAATCTGCAATATTTAT 571
 567 ACTGCGTACACATATTCAGAGAGACATTTCTGGATTACATTAATCTAATTAATCTGT 626
 572 ATCTCAACCAACATGTCATCAG 593
 627 ATTCAGCCATTAATGTCATTAAC 648

RESULT 5

LOCUS

DEFINITION

EX084029 758 bp mRNA linear EST 25-APR-2003
 (tcac) Oncorhynchus mykiss cDNA clone tcac0004c.h.01 5prim, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oncorhynchus mykiss (rainbow trout)
 Oncorhynchus mykiss
 Bkayota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Govoroun, M., Guiguen, Y. and Le Gac, F.
 Construction and primary characterization of normalized cDNA
 libraries in rainbow trout, *Oncorhynchus mykiss*
 unpublished
 Contact: Guiguen Y

INRA - SCRIBE
 Campus de Beaulieu, RENNES cedex, 35042, France
 Tel: 02.23.48.50.09
 Fax: 02.23.48.50.20
 Email: Yann.Guiguen@beaulieu.rennes.inra.fr
 Sequence cleaned of vector, adaptor and repetitions. Contact us
 at sigenae@port@jouy.inra.fr to obtain the chromatogram of this
 sequence.
 Plate: 0004 row: h column: 1
 Seq primer: 17.
 Location/Qualifiers

FEATURES

source

1..758

/organism="Oncorhynchus mykiss"

/mol_type="mRNA"

/db_xref="taxon:8022"

/clone="tcac0004c.h.01"

/tissue_type="adipose tissue, blood, brain,
 differentiating gonads, gills, intestinal, intestine,
 kidney, liver, muscle, ovary, pituitary, testis"

/dev_stage="from embryos to adults"

/lab_host="VDH10B"

/clone_lib="AGENAE Rainbow trout normalized multi-tissues
 library (tcac)"

/note="Vector: pRT73D-pac; Clone distribution: AGENAE
 Resource centre. Francois Pluim,
 Francois Pluim@jouy.inra.fr, INRA, CEA Radiobiologie et
 Brûle du genome (IREG), Domaine de Vilvert, 78352,
 Jouy-en-Josas cedex, France"

BASE COUNT 165 a 217 c 178 g 198 t

Query Match

Best Local Similarity 13.5%; Score 306.2; DB 13; Length 758;

Matches 446; Conservative 0; Mismatches 233; Indels 0; Gaps 0;

1491 CATGGGTTCTGGCCATGCTGTCAACGAGTCTGTGTTCTGCTACTGACTTATGAC 1550
 8 CATGGGTTCTGGCCATGCTGTCTCTCAGAGTATCTGTGCTGCTGACTTACTGAC 67
 1551 TTTGGAGAGTCCGCGTATGCTCTCCCTTCAGTAATTCGACCTGAGAAACGGA 1610
 68 TGTGGAGAGTCCGCGTATGCTCTCTCAGAGTATCTGTGCTGCTGACTTACTGAC 127
 1611 GACCTGATCATCTCATTTGATGCTGTGAGCGGATTTTAAAGCTGAATTCAT 1670
 128 GACTGCGGTGCTGTTATCTATCTGCGGTGCTGAGTTCATCTGCGGTGCTGCT 187
 1671 TTGAATTAAGATTATTTGAAACTTTTATGAGAAAAATGAGATATGTTCCACTTA 1730
 188 GATGAACGAGACTGTGTTGGAAGTACTATGTTGTAACGGGCTGCTTCCCTTACA 247
 1731 TTATGACCAACAGAAATATTGAAGCAAGGATTTCTTGAATTTTCTAGAGT 1790
 248 CTCTGACAGACAGAGAAAGCCCACTGCTAAAGATCTTATTCGATTTCTGAGT 307
 1791 GAATGCTGCGTCTTCTCATCATTTGTTTCTCATATTAATTAATTAATTAATTAAT 1850
 308 GAACCTGCGAGATTTCTGATGATGATGTTCTTACTCTCCAGATTTCTACTCATTA 367
 1851 AAAAAACGCTTGCAGACCAAGAAATTAAGAAATTTTGAAGAGAGAGTGGCTTTC 1910
 368 CAAGATGATTAACAGCTACAGACCTGAGAGAGCTACACAGAGAGTGGCTTTC 427
 1911 AATGCTTCTTTTATATGATGTTCTGATGCTGATGCTGATGCTGATGCTGATGCT 1970
 428 TAAAGTCTTCTTCAATGTTCTTCTGACGCTCTGCTGATGCTGATGCTGATGCT 487
 1971 TAAATCTTCTTCTTCTTCTGCGGTGAGAAATACAGACATGATCTTCTGATGAT 2030
 488 CAAGATGATGCTGCTGCTGAGAGTACAGATGATGATGATGATGATGATGATGAT 547
 2031 TTTTCTTCTGAGTAAAGGCTTGAATCAATCTCTTAATCTCTGACAAACCACT 2090

from normal endometrial tissue (mid-secretory phase, cycle day 23). Average insert size 1.6 kb. Library constructed by RegGen (Invitrogen Corporation)."

BASE COUNT

180 a 112 c 133 g 223 t

ORIGIN

Query Match 12.8%; Score 290.2; DB 14; Length 648;
Best Local Similarity 65.5%; Pred. No. 7.7e-51;
Matches 424; Conservative 0; Mismatches 223; Indels 0; Gaps 0;

QY 1255 AGAATATTTGTCGGGTATAGCTTTCATTAAGCTGCTTTGGAAATCTTTTGTGATGGC 1314
DB 2 AGAGTATTTGTCGGGTATAGCTTTCATTAAGCTGCTTTGGAAATCTTTTGTGATGGC 61
QY 1315 ATGAGATCTTTCATTAAGCTGAAATATCAACTCAGCTATGCTATGCAATTAATCTTTG 1374
DB 62 ATGCACTTATATTCAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAGGTCGAG 121
QY 1375 TGTGCTGATTCCTGATGAGGTCGATTCCTGCTTTGTTGGCAATTTTCATTAATATAC 1434
DB 122 TGTGCGGAGCTGCTTAATGGAATATATTTATTCGATGAGGCTTTGACCTAAAGTTT 181
QY 1435 CGAGGCAATATCAAGATATGCTTCTGCTGATGAGGTCGAGGTCGAGGTCGAGGTCGAG 1494
DB 182 CGTGAGAAATACATTAAGCATGCGCAGCTGTGAGAGTCTCATTTGTCAGCTTGTGA 241
QY 1495 GGGTCTGCGGCAATGCTGCTGCAAGGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1554
DB 242 GATCTTTGGCCATTTCTGTCACAGAAATATCAATTTTACATTTTCTGACATTTG 301
QY 1555 GAGAAATTCCTGATGCTTCTTCCCTTCAATGATGATGATGATGATGATGATGATGATG 1614
DB 302 GAAATATATCATGCAATGCTTCTTAAATGATGATGATGATGATGATGATGATGATGATG 361
QY 1615 TCAATATCTCATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1674
DB 362 ATTAAGTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 421
QY 1675 AATAAGATATTTTGAATCTTTTATGGAATATGATGATGATGATGATGATGATGATGATG 1734
DB 422 AATAAGATATTTTGAATCTTTTATGGAATATGATGATGATGATGATGATGATGATGATG 481
QY 1735 GACCAACAGAGATATTTGAGCAAGGATTTCTTGGAAATTTTCTTGAATGATGATG 1794
DB 482 GAAGATACAGAAATATTTGAGCAAGGATTTCTTGGAAATTTTCTTGAATGATGATG 541
QY 1795 TTTGCTGCTTTCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1854
DB 542 TTTGCTGCTTTCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 601
QY 1855 ACCGCTTTCAGACACAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1901
DB 602 AGTGCCATACAGCACTGAAATACGAAATCAAGTTAAAAAGAGAT 648

RESULT 8

AV592705 461 bp mRNA linear EST 27-NOV-2001

LOCUS

AV592705 Bos taurus cartilage fetus Bos taurus cDNA clone

DEFINITION

AV592705 3', mRNA sequence.

ACCESSION

AV592705

VERSION

AV592705.1 GI:9707862

KEYWORDS

EST.

SOURCE

Bos taurus (cow)

ORGANISM

Bos taurus (cow)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.

REFERENCE

1 (Bases 1 to 461)
Takaue, A., Hirotsune, S., Itoh, R., Jitohzono, A., Suzuki, H., Aso, H.
Establishment of a high throughput EST sequencing system using
poly(A) tail-removed cDNA libraries and determination of 36,000

bovine ESTs
Nucleic Acids Res. 29 (22), E108 (2001)
MEDLINE 21570554
PubMed 11713328
COMMENT
Contact: Yoshikazu Sugimoto
Animal Genetics Division
Shirakawa Institute of Animal Genetics
Odakura, Nishigo, Nishik-shirakawa, Fukushima 961-8061, Japan.
Tel: 81-248-25-5641
Fax: 81-248-25-5725
Email: kazusugi@ccoc.ocn.ne.jp

Single pass sequencing.
This clone was obtained from a polyA-deleted cDNA library.

FEATURES

source

1..461
/organism="Bos taurus"
/mol_type="mRNA"
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/clone="E1CA03B08"
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/lab_host="DH10B"
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/note="vector: pZ1; Site_1: SalI; Site_2: NotI; Poly A
was deleted from a NotI site"

BASE COUNT

134 a 104 c 109 g 109 t 5 others

ORIGIN

Query Match 12.8%; Score 288.8; DB 9; Length 461;
Best Local Similarity 87.0%; Pred. No. 1.5e-50;
Matches 314; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

QY 1433 ACCGAGGCAATATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1492
DB 460 ACCGAGGCAATATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 401
QY 1493 TGGGCTCTGCGCATGCTGTCACCGAAGTCTGTTCTGCTGCTGCTGCTGCTGCTGCTG 1552
DB 400 TGGGCTCTGCGCATGCTGTCACCGAAGTCTGTTCTGCTGCTGCTGCTGCTGCTGCTG 341
QY 1553 TGGAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1612
DB 340 TGGAGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 281
QY 1613 CCTGATCATCTCATTTTGCATCTGAGATGAGGATTTTATAGCTGATTTTCAATTT 1672
DB 280 CCTGATCATCTCATTTTGCATCTGAGATGAGGATTTTATAGCTGATTTTCAATTT 221
QY 1673 GGAATTAAGATATTTTGAATCTTTTATGGAATATGATGATGATGATGATGATGATG 1732
DB 220 GGAATTAAGATATTTTGAATCTTTTATGGAATATGATGATGATGATGATGATGATG 161
QY 1733 ATGACCAACAGAGATATTTGAGCAAGGATTTCTTGGAAATTTTCTTGAATGATG 1792
DB 160 ATGACCAACAGAGATATTTGAGCAAGGATTTCTTGGAAATTTTCTTGAATGATG 101

RESULT 9

AM307854 300 bp mRNA linear EST 25-APR-2001

LOCUS

AM307854 1346 MARC 4BOV Bos taurus cDNA 5', mRNA sequence.

ACCESSION

AM307854

VERSION

AM307854.1 GI:6720217

KEYWORDS

EST.

SOURCE

Bos taurus (cow)

ORGANISM

Bos taurus (cow)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 300)
 AUTHORS Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
 Casass,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,
 G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-Mckom,C.G.,
 Pettea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and
 Keefe,J.W.
 TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA
 JOURNAL libraries and construction of a gene index for cattle
 MEDLINE Genome Res. 11 (4), 626-630 (2001)
 PUBMED 21180013
 COMMENT 11282978
 Contact: Smith TPL
 USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390
 Email: smith@email.marc.usda.gov
 Single pass sequencing. Bases called and trimmed with phred
 v0.980904.e. Vector identified by cross_match with the -minscore 20
 and -mismatch 12 options.
 PCR Primers
 FORWARD: AGGAACAGCTATGACAT
 BACKWARD: GTTTCACAGCAGACG
 Plate: 142 row: H column: 17
 Seq primer: ATTAGTGACACTATAG.
 Location/Qualifiers
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 /tissue_type="pooled"
 /lab_host="DH10B"
 /clone_id="DMC 4BOV"
 /note="Vector: PCMV SPORT6; Site 1: NotI; Site 2: SalI;
 library made from pooled tissue from day 20 and day 40
 embryos."

BASE COUNT 62 a 69 c 74 g 95 t
 ORIGIN

Query Match 11.4%; Score 257.4; DB 9; Length 300;
 Best Local Similarity 91.3%; Pred. No. 6.6e-44;
 Matches 273; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 1203 CTTCAGCAGCGCATTTCTTCATTGAGACCTCTTGCTTAACAATATCTCAGATATT 1262
 DB 2 CTTCAGCAGCGCATTTCTTCATTGAGACCTCTTGCTTAACAATATCTCAGATATT 61
 QY 1263 TGTCTGGTTATAGCTTTGATTAACCTGCTTTGGAATCTTTTGTGATGCGATGATC 1322
 DB 62 TGGCTGGTTATAGCTTTGATTAACCTGCTTTGGAATCTTTTGTGATGCGATGATC 121
 QY 1323 TTTTCATTAAGCTGAATAATACAACTCAGCTATGTCATCAAAATCTTTGTTGTGCTGA 1382
 DB 122 TTTTCATTAAGCTGAATAATACAACTCAGCTATGTCATCAAAATCTTTGTTGTGCTGA 181
 QY 1383 TTGCTGATGGGTGTTACTGTTCTTTGTTGTGAGATTTCATTAATAATACCGAGGCA 1442
 DB 182 CTGCTGATGGGTGTTACTGTTCTTTGTTGTGAGATTTCATTAATAATACCGAGGCA 241
 QY 1443 GTATCAGAGTATGCTTCTGCTGATGAGAGCGGCGATGCCGCTCATGGGCTTC 1501
 DB 242 GTATCAGAGTATGCTTCTGCTGATGAGAGCGGCGATGCCGCTCATGGGCTTC 300

RESULT 10
 A0394779 549 bp DNA linear GSS 06-MAR-1999
 LOCUS CITR1-El-2548P17.TR CITR1-El Homo sapiens genomic clone 2548P17,
 DEFINITION genomic survey sequence.
 ACCESSION A0394779
 VERSION A0394779.1 GI:4365802
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 549)
 AUTHORS Zhao,S., Adams,M.D., Niernan,W., Malek,J., Shizuya,H., Simon,M. and
 Venter,J.C.
 TITLE Use of BAC End Sequences from Caltech Libraries for Sequence-Ready
 JOURNAL Map Building
 COMMENT Unpublished
 Other GSSs: CITR1-El-2548P17.TF
 Contact: Shaying Zhao, William Niernan, Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: hbo@tigr.org
 Clones are available from Research Genetics (info@resgen.com). BAC
 end search page:
 http://www.tigr.org/cdb/humgen/bac_end_search/bac_end_search.html.
 Seq primer: M13 Reverse
 Class: BAC ends.

FEATURES
 source Location/Qualifiers
 1..549
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 /db_xref="taxon:9606"
 /clone="2548P17"
 /sex="male"
 /cell_type="sperm"
 /clone_id="CITR1-El"
 /note="Vector: pBelobAC11; Site_1: EcoRI; Site_2: EcoRI;
 Caltech Human BAC Library D"

BASE COUNT 152 a 110 c 96 g 189 t 2 others
 ORIGIN

Query Match 10.1%; Score 228.8; DB 28; Length 549;
 Best Local Similarity 98.3%; Pred. No. 7.9e-38;
 Matches 230; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1144 ATTTATTCAAAATCTTGATGATGCTGCTGATGCTCCCATGTCGATATGATGCCC 1203
 DB 226 ACTATATTCAAAATCTTGATGATGCTGCTGATGCTCCCATGTCGATATGATGCCC 285
 QY 1204 TTGACGAGCGCATTTCTTCATTGAGACCTCTTGCTTAACAATATCTCAGATATT 1263
 DB 286 TTGACGAGCGCATTTCTTCATTGAGACCTCTTGCTTAACAATATCTCAGATATT 345
 QY 1264 GTCTGGTTATAGCTTTGATTAACCTGCTTTGGAATCTTTTGTGATGCGATGATC 1323
 DB 346 GTCTGGTTATAGCTTTGATTAACCTGCTTTGGAATCTTTTGTGATGCGATGATC 405
 QY 1324 TTTTCATTAAGCTGAATAATACAACTCAGCTATGTCATCAAAATCTTTGTTGTGCTGA 1377
 DB 406 TTTTCATTAAGCTGAATAATACAACTCAGCTATGTCATCAAAATCTTTGTTGTGCTGA 459

RESULT 11
 BF040869 279 bp mRNA linear EST 10-OCT-2000
 LOCUS BP25001A10B3 Soares normalized bovine placenta Bos taurus cDNA
 DEFINITION Clone BP25001A10B3 5', mRNA sequence.
 ACCESSION BF040869
 VERSION BF040869.1 GI:10757924
 KEYWORDS EST.
 SOURCE Bos taurus (cow)
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovidae; Bovinae; Bos.
 REFERENCE 1 (bases 1 to 279)
 AUTHORS Lewin,H.A., Soares,M.B., Rebeiz,M., Pardinas,J., Liu,L. and Larson,
 J.H.

JOURNAL TITLE	COMMENT
Unpublished Bovine ESTs	
Contact: Lewin, H. A.	
W. M. Keck Center for Comparative and Functional Genomics	
University of Illinois at Urbana-Champaign	
340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL 61801, USA	
Tel: 217 333 5998	
Fax: 217 244 5617	
Email: h-lewin@uiuc.edu	
Funding for cattle EST sequencing was provided by the USDA National Research Initiative, Animal Genome Resource Grant AG 99-3205-8534 to H. A. Lewin and J. B. Womack. Base Calling/Quality Scores: PHRED from Washington University Genome Center. Vector Trimmi g: Cross match from Washington University Genome Center PHRAP suite. This sequence is vector free and at least 200 bp in length.	
PCR primers	
FORWARD: TAAACGACCTCATTATAGGG	
BACKWARD: ATTAACCTCCTCATTAAAG	
Insert Length: 279 Std Error: 0.00	
Plate: BP250001A10 row: B column: 3	
Seq primer: AGCGGATACCAATTTCACACAGGA	
High quality sequence stop: 279.	
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/clone="BP250001A10B3"	
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/lab_host="DH10B"	
/clone_11b="Soares normalized bovine placenta"	
/note="Organ: Placenta; Vector: pT73pac; Site 1: EcoRI; Site 2: NotI; The cDNA library was contributed by the Soares laboratory and it was constructed and normalized as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806."	
M.B. (1996), Genome Research 6(9): 791-806."	
BASE COUNT	
51 a 75 c 70 g 83 t	
ORIGIN	
Query Match	
Best Local Similarity 9.9%; Score 224.6; DB 10; Length 279;	
Matches 245; Conservative 0; Mismatches 34; Indels 0; Gaps 0;	
QY 1306 GTGATTGGGATGAGTCTTTCTATTAAAGCTGMAAATACAACTACGCTATGTCCATCAA 13655	
DB 1 GTGATTGGGATGAGTCTTTCTATTAAAGCTGMAAATACAACTACGCTATGTCCATCAA 60	
QY 1366 ATCCCTTATGTGCGATTGCTGCTAGTGGGTGTTTACTTGTCTTGGGATTTTCAT 1425	
DB 61 ATCCCTTGTGCGGACTGCTGTAAGGTGTGTATCTGTCTTATTTGGCCCTTTGGCAT 120	
QY 1426 ATAAATAACGAGGCGAGTATCAGAAAGTATGCTTGTCTGTGATGAGAGCGTGCATGTC 14859	
DB 121 CTAAAGTACCGAGGCGAGTATCAGAAAGTATGCTTGTCTGTGATGAGAGCGTGCATGTC 180	
QY 1486 CGCCTTCATGGGGTCTTCTGAGCCATGCTGTTCACCGAAGTCTCTGTCTGCTACTGACCTAC 15454	
DB 181 CGCCTTCATGGGGTCTTCTGAGCCATGCTGTTCACCGAAGTCTCTGTCTGCTACTGACCTAC 240	
QY 1546 TTGACTTTGAGAGAAGTCTCTGTGTCATTTGCTTCCCTTC 1584	
DB 241 TTGACCTCTGAGAGAAGTCTCTGTGTCATTTGCTTCCCTTC 279	
RESULT 12	
BU366143	857 bp mRNA linear EST 28-NOV-2002
LOCUS	
DEFINITION	603585541F1 CSEQCCHN2 Gallus gallus cDNA clone ChST51a11 5', mRNA
ACCESSION	BU366143
VERSION	BU366143.1
KEYWORDS	GI:25874144

SOURCE	ORGANISM
Gallus gallus (chicken)	
Gallus gallus	
Eukaryote: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;	
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;	
Phasianinae; Gallus.	
1 (bases 1 to 857)	
Boardman, P.E., Sant-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,	
Pong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.	
A Comprehensive Collection of Chicken CDNs	
Curr. Biol. 12 (22), 1965-1969 (2002)	
22335534	
12445392	
Contact: Simon Hubbard	
Department of Biomolecular Sciences	
University of Manchester Institute of Science and Technology (UMIST)	
)	
PO Box 88, Manchester, M60 1QD, UK	
Tel: 01612008930	
Fax: 01612360409	
Email: Simon.Hubbard@umist.ac.uk.	
Location/Qualifiers	
1..857	
/organism="Gallus gallus"	
/mol_type="mRNA"	
/strain="Compton Line 151"	
/db_xref="taxon:9031"	
/clone="CHES7541a11"	
/sex="Female"	
/tissue_type="cerebrum"	
/dev_stage="adult"	
/lab_host="DH10B"	
/clone_id="CSEQCHN72"	
/note="Organ: brain; Vector: pBluescript II KS(+); Site: 1;	
ECORI; Site 2: NotI; This normalized library was	
constructed from 1 million independent clones. cDNA	
synthesis was initiated using an oligo(dT) primer, using	
methyalted C in the first strand synthesis reaction.	
Following this first strand reaction, double-stranded cDNA	
was bluntend, ligated to NotI adapters, digested with EORI	
, size-selected, and cloned into the NotI and EORI	
compatible sites of a custom modified MCS of the	
pBluescript (KS+) vector. The library was normalized in 2	
rounds using conditions adapted from Soares et al., PNAS	
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6	
(1996): 791, except that a significantly longer	
reannealing hybridization was used."	
reannealing hybridization was used."	
BASE COUNT	259 a 191 c 167 g 240 t
ORIGIN	
Query Match	8.4%; Score 190.6; DB 13; Length 857;
Best Local Similarity	54.2%; Pred. No. 1e-29; Matches 354; Indels 22; Gaps 2
Matches	445; Conservative 0; Mismatches 354; Indels 22; Gaps 2
Db	108 TCAGGTGACATGATCACTCTTCATGACCAAAAGATATTTTCCCTGTGGAAATCTAC 167
Qy	23 TCCTGTTCCAGAGCGGTGCTGCTGCTGCCCTTGGGCTACCTTCCCTGTGGCAATATCAC 82
Db	168 CAATGCTTACCCGAGCTTTTCACTGTGATGCGCAAGATGACTGTGGAAACGGGGCCGA 227
Qy	83 AAAGGCTTGGCCCAACAATCTCACTGTAATGGTGAAGATGACTGTGGAAATCATGCTGA 142
Db	228 CGAAGAGAAGCTGTGTGACACTAGTGAATGGGCGACATATTTGGGCAAGTGCATGAA 287
Qy	143 TGAAGACAACGTGTGAAGCAACAATGATGTGTCTTACAATTGACAACATTCACATTT 202
Db	288 TGCTTAACA-----GCTGGCTTTAACAACAAGAGTCTTTCTTAACAACA 329
Qy	203 AGACAAATGAAATCCCTGTACGCAATTCAGACCAAGACACAGAGTCCCTGGCGGTGC 262
Db	330 GTATCCAAAGCTGTGACGTGAAGAAAGCAATGGAATGTGAATGGTGAATGGAATTTAA 389
Qy	263 TGTACCAATGAAATTAATGCAAGGCTGAGGTCTTCTGTATGCTGCCAAACTGCG 322


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Db      295 TGGCGAATACACCGGAGCGCTGTGATCTGATGAGAGAGCGTTGAATGCCGAACATTTGG 354
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Db      355 CTTTCCTGGCAGCTCTCTCCCTGAGAGCTGCTGCTCTCTCCCTCACTTGAATTAAGA 414
QY      1557 GAAGTCTGGGATATGTTCTTCCCTTCAGTACATTCGACCGGAAAACGGAGACCTTC 1616
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QY      1617 AGTCACTCTCATTTGATCTGATGAGCGGATTTTAAATGCTGTAATTCATTTGGA 1676
Db      475 GCGATCTTGGCTTATCTGATCTGCTGAGATTTGATGACGCTGTTCCCTGTTAA 534
QY      1677 TAAGATTTATTTGGAACCTTTTATGGAATAATGAGATGTTTCCCACTTATTAAGA 1736
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QY      1737 CCAACGAAATATTTGGAAGCAAGGGATTTCTCTTGAATTTTCTAGTGTGA 1792
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RESULT 15

A2319928/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

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A2319928      532 bp      DNA      linear      GSS      29-SEP-2000
LOCUS      1M0039D13R      Mouse 10kb plasmid UUCGM library Mus musculus genomic
DEFINITION      clone UUCGM0039D13 R, genomic survey sequence.
ACCESSION      A2319928
VERSION      A2319928.1      GI:10371193
KEYWORDS      GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
REFERENCE      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE      1 (bases 1 to 532)
JOURNAL      Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamil, C.,
COMMENT      Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
      M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
      Mouse whole genome scaffolding with paired end reads from 10kb
      plasmid inserts
      Unpublished
      Contact: Robert B. Weiss
      University of Utah
      University of Utah
      Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
      84112, USA
      Tel: 801 585 5606
      Fax: 801 585 7177
      Email: ddunn@genetics.utah.edu
      Insert Length: 10000      Std Error: 0.00
      Plate: 0039      row: D      column: 13
      Seq primer: CACACAGGAAACAGCTATGACC
      Class: plasmid ends
      High quality sequence stop: 532.
      Location/Qualifiers
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          /organism="Mus musculus"
          /mol_type="genomic DNA"
          /strain="C57BL/6J"
          /db_xref="taxon:10090"
          /clone="UUCGM0039D13"
          /sex="Male"
          /lab_host="E. Coli strain XL10-Gold, Ti-resistant, F-"
          /clone_lib="Mouse 10kb plasmid UUCGM library"
          /note="Vector: PWD42nv; Purified genomic DNA from M.
          musculus C57BL/6J (male) was obtained from the Jackson
          Laboratory Mouse DNA Resource
          (http://www.jax.org/resources/documents/dnares/). The DNA
          was hydrodynamically sheared by repeated passage through a
          0.005 inch orifice at constant velocity. The sheared DNA
          was blunt end-repaired with T4 DNA polymerase and T4

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polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid RL. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT

184 a 120 c 95 g 133 t

ORIGIN

Query Match 8.3%; Score 188.6; DB 28; Length 532;
 Best Local Similarity 87.7%; Pred. No. 2.6e-29;
 Matches 206; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

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QY      1143 CATTTATTTCAAAACTTTCGATGCTGCTCCATGCTCCCATGTCGGAATATGATGCG 1202
Db      511 CAGTATTTGAAACCTTCGATGCTGCTCCATGCTCCCATGTCGGAATATGATGCG 452
QY      1203 CTGACGAGCGCATTCTTTCATTTGAGGACCTTTGCTAACAATATCTCAGAAAT 1262
Db      451 GTGACGTATGATGATTTCTGCTGAGGACCTTTGCTAACGATCTCAGAGTGC 392
QY      1263 TGTCTGGGTTATGACTTTTATTAACCTGCTTGGAAATCTTTTGTTCATTTGCA 1322
Db      391 TGTCTGGGTTATGACTTTTATTAACCTGCTTGGAAATCTTTTGTTCATTTGCA 332
QY      1323 TTTTCATTAAGCTGAAATATCAACTCAGCTATGTCATCAAAATCTTGTGT 1377
Db      331 TCTCATTAAGCTGAAATATCAACTCAGCTATGTCATCAAAATCTTGTGT 277

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Search completed: November 28, 2003, 19:17:04
 Job time : 4266 secs

Db 301 CATTAGCTGATACCATTTTGTAGTAAATTTCTTACCTGCTTCAAGTAATAC 360
Qy 2003 CAGACCAATGACTCTCTGATAGTATTTTCTTCCAGTTACAGCTTTGATC 2062
Db 361 CAGGTACCATACCTCTGGGTAGTATTTTATCTGCCCATTACAGAGCTTTGAAC 420
Qy 2063 CAATCCCTTACTCTTACCAACCACTTTTAAAGCAAGTTGAACAGCTGCTGACA 2122
Db 421 CAATCTCTTACTCTGACCAAGACCATTTTAAAGAAATGATTCATGCGTTTGTATA 480
Qy 2123 AACCA---TCAGAGGAATCAATTTTCAAAATTAATAAAAGTTTACTACATCCATG 2179
Db 481 ACTACACACAAAGAAATCTATGACAGCAAGCTCAGAAACATATGCTCATCATCA 540
Qy 2180 TGTGATAGA 2189
Db 541 TCTGGGTGGA 550

RESULT 2
US-08-487-886-1
; Sequence 1, Application US/08487886
; Patent No. 5744448
; GENERAL INFORMATION:
; APPLICANT: Kelton, Christie Ann
; APPLICANT: Schweichardt, Rene Lynn
; APPLICANT: Cheng, Shirley Vui Yen
; APPLICANT: Nugent, No. 5744488en Patrice
; TITLE OF INVENTION: Human Follicle Stimulating
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stephan P. Williams,
; ADDRESS: Ares-Serono, Inc.
; STREET: Exchange Place, 37th floor
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" diskette, 1.44 MB, high density
; COMPUTER: IBM PS/2, model 55 SX
; OPERATING SYSTEM: MS-DOS version 4.0
; SOFTWARE: VAX/VMS Mas811 via Kermit to IBM MS-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,886
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/670,085
; FILING DATE: 15-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams, Stephan P.
; REGISTRATION NUMBER: 28546
; REFERENCE/DOCKET NUMBER: US/252
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 723-1300
; TELEFAX: (617) 723-8923
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2179
; TYPE: Nucleic acid
; STRANDEDNESS: Double
; TOPOLOGY: Linear
; MOLECULE TYPE: cDNA to mRNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; TISSUE TYPE: Testis
; IMMEDIATE SOURCE:
; LIBRARY: 1g11 cDNA library, Clontech #HL1010b
; CLONE: pHPShr11-11, pHPShr15-6
; FEATURE:

NAME/KEY: protein coding region
; LOCATION: 75 to 2159
US-08-487-886-1

Query Match 2.8%; Score 63.6; DB 1; Length 2179;
Best local similarity 47.3%; Pred. No. 3.1e-08;
Matches 192; Conservative 0; Mismatches 214; Indels 0; Gaps 0;

Qy 1166 ACTGCTCTATGCTCCCATGTCGAATATGATAGCCCTTGACGAGCGGATTTCTCAT 1225
Db 1081 ACTTATGACATAGTAGGTGAGCTGACCTGCTCCCTTAAGCCAGATTCACACCAT 1140
Qy 1226 TTGAGGACCTCTGAGTAACAATATCTCAGATATTTGCTGGTTATAGCTTTCACTA 1285
Db 1141 GTGAAATATCATGGGATCAACATCTCAGAGCTCTGATATGTTATACAGATCTCG 1200
Qy 1286 CCTGCTTGGAAATCTTTTGTGATGTCAGATAGATCTTTCAATTAAGCTGAATAACAA 1345
Db 1201 CCATCACTGGAAACATATAGTGTATGATCTTAATCAACGCCAATATTAACCTCAG 1260
Qy 1346 CTGACGCTATGTCATCAAAATCTTTGTTGCTGATGCTCCGATGGGTTTACTGT 1405
Db 1261 TCCCAAGTTCCTTATGTCACACCTGGCCTTGTGATCTGCAATGAAATCTTACCTC 1320
Qy 1406 TCTTGTGACATTTTCGATATTAATAACGAGGCGAGTACAGAAATGCTTGTCTGT 1465
Db 1321 TGCTATTCATCATAGTATATTCATACCAAGGCCAATATCAACTATGCAATGACT 1380
Qy 1466 GGATGAGAGCGTGCAGTGCCTGCTCATGGGTTCTTGCCATCTGTCCAGCAAGTCT 1525
Db 1381 GCGAAACTGGGGAGGCGCTGTGATGTCGCTGCTTTTCACTGCTTTGCGCAGTACGT 1440
Qy 1526 CTGTTGCTACTGACCTACTGACTTTTGAGAGAGTTCTGGTCAAT 1571
Db 1441 CAGTCACTCTGACAGCTATACCTTGAAAGATGGCATACCAT 1486

RESULT 3
US-08-531-070A-1
; Sequence 1, Application US/08531070A
; Patent No. 5851768
; GENERAL INFORMATION:
; APPLICANT: de la Chapelle, Albert
; APPLICANT: Altomaki, Kristina
; APPLICANT: Hubblaniemi, Ilpo
; TITLE OF INVENTION: Method For Diagnosis Of Ovarian Dysgenesis
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/531,070A
; FILING DATE: 20-SEP-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gass, David A.
; REGISTRATION NUMBER: 38,153
; REFERENCE/DOCKET NUMBER: 28113/32879
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:

LENGTH: 2179 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-531-070A-1

Query Match 2.8%; Score 63.6; DB 2; Length 2179;
Best Local Similarity 47.3%; Pred. No. 3.1e-08;
Matches 192; Conservative 0; Mismatches 214; Indels 0; Gaps 0;

1166 ACTGCTCTATGCTCCCATGTCGAATATGATGCTTGAACGAGCAATTTCTTAT 1225
1081 ACTATGCAATGAAGTGTATGACGACCTGCTCCCAAGCCAGATCATTCACCAT 1140
1226 TTGAGACCTCTGGCTTACATATATCTCAGAAATTTGTCTGGGTATTAAGCTTATTA 1285
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1286 CTGCTTGGAAATCTTTTGTCTATGTCAGATGAGATCTTTCAATTAAGCTGAATAACA 1345
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1346 CTCACGCTATGCTCAAAATCTTGTGTGCTGATGCTGATGAGGTGTTACTGT 1405
1261 TCCCAAGTCTCTATATGCAACCTGACCTTGTGATCTGCAATGGAATCTACCTGC 1320
1406 TCTTTTGGCATTTTCATATATAATACGAGGCGAGTATCAGAAATGCTTGTCTGT 1465
1321 TGTCTATGATCATGATGATATATCCATACAGAGCCAAATATCACAATGATGACT 1380
1466 GGATGAGAGGCTGACAGTCCGCTCATAGGGGTCTTGGCCATGCTGTCCACCGAAGCT 1525
1381 GGCAAACTGGGGCAGGCTGTGATGCTGCTGCTTTTCACTGTCTTGTCCAGTGAAGCTGT 1440
1526 CTGTTCTGCTACTGACCTACTTGAATTTGAGAAATGCTGAT 1571
1441 CAGCTTACACTGTGACGACTATCAGCTTGAAGATGCAATCAAT 1486

RESULT 4
US-08-482-855-1
Sequence 1, Application US/08482855

PATENT No. 6121016
GENERAL INFORMATION:
APPLICANT: Kelton, Christie Ann
APPLICANT: Schweickhardt, Rene Lynn
APPLICANT: Cheng, Shirley Vui Yen
APPLICANT: Nugent, No. 6121016en Patrice
TITLE OF INVENTION: Human Follicle Stimulating
TITLE OF INVENTION: Hormone Receptor
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephan P. Williams,
ADDRESSEE: Ares-Serono, Inc.,
STREET: Exchange Place, 37th floor
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" diskette, 1.44 MB, high density
COMPUTER: IBM PS/2, model 55 SX
OPERATING SYSTEM: MS-DOS version 4.0
SOFTWARE: VAX/VMS Mase11 via Kermit to IBM MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482, 855
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/670, 085
FILING DATE: 15-MAR-1991
ATTORNEY/AGENT INFORMATION:

NAME: Williams, Stephan P.
REGISTRATION NUMBER: 28546
REFERENCE/DOCKET NUMBER: US/252
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 723-1300
TELEFAX: (617) 723-8923
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2179
TYPE: Nucleic acid
STRANDEDNESS: Double
TOPOLOGY: Linear
MOLECULE TYPE: CDNA to mRNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
TISSUE TYPE: Testis
IMMEDIATE SOURCE:
LIBRARY: 19711 CDNA Library, Clontech #HL1010b
CLONE: pF5HR11-11, pF5HR15-6
FEATURE:
NAME/KEY: protein coding region
LOCATION: 75 to 2159
US-08-482-855-1

Query Match 2.8%; Score 63.6; DB 3; Length 2179;
Best Local Similarity 47.3%; Pred. No. 3.1e-08;
Matches 192; Conservative 0; Mismatches 214; Indels 0; Gaps 0;

1166 ACTGCTCTATGCTCCCATGTCGAATATGATGCTTGAACGAGCAATTTCTTAT 1225
1081 ACTATGCAATGAAGTGTATGACGACCTGCTCCCAAGCCAGATCATTCACCAT 1140
1226 TTGAGACCTCTGGCTTACATATATCTCAGAAATTTGTCTGGGTATTAAGCTTATTA 1285
1141 GTGAAGATATCATGGGGTACAAACATCTCAGATCCTATATGTTTATGACATCTCG 1200
1286 CTGCTTGGAAATCTTTTGTCTATGTCAGATGAGATCTTTCAATTAAGCTGAATAACA 1345
1201 CCATCACTGGGAAACATCATGAGTATGATCTTAATACAGCCAAATATAAAGTCAAG 1260
1346 CTCACGCTATGCTCAAAATCTTGTGTGCTGATGCTGATGAGGTGTTACTGT 1405
1261 TCCCAAGTCTCTATATGCAACCTGACCTTGTGATCTGCAATGGAATCTACCTGC 1320
1406 TCTTTTGGCATTTTCATATATAATACGAGGCGAGTATCAGAAATGCTTGTCTGT 1465
1321 TGTCTATGATCATGATGATATATCCATACAGAGCCAAATATCACAATGATGACT 1380
1466 GGATGAGAGGCTGACAGTCCGCTCATAGGGGTCTTGGCCATGCTGTCCACCGAAGCT 1525
1381 GGCAAACTGGGGCAGGCTGTGATGCTGCTGCTTTTCACTGTCTTGTCCAGTGAAGCTGT 1440
1526 CTGTTCTGCTACTGACCTACTTGAATTTGAGAAATGCTGAT 1571
1441 CAGCTTACACTGTGACGACTATCAGCTTGAAGATGCAATCAAT 1486

RESULT 5
US-08-474-986-1
Sequence 1, Application US/08474986

PATENT No. 6372711
GENERAL INFORMATION:
APPLICANT: Kelton, Christie Ann
APPLICANT: Schweickhardt, Rene Lynn
APPLICANT: Cheng, Shirley Vui Yen
APPLICANT: Nugent, No. 6372711en Patrice
TITLE OF INVENTION: Human Follicle Stimulating
TITLE OF INVENTION: Hormone Receptor
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stephan P. Williams,
ADDRESSEE: Ares-Serono, Inc.,
STREET: Exchange Place, 37th floor

CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" diskette, 1.44 MB, high density
COMPUTER: IBM PS/2, model 55 SX
OPERATING SYSTEM: MS-DOS version 4.0
SOFTWARE: VAX/VMS Mass81 via Kermit to IBM MS-DOS

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,986
FILING DATE: 07-Jun-1995
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/670,085
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Williams, Stephen P.
REGISTRATION NUMBER: 28546
REFERENCE/DOCKET NUMBER: US/252
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 723-1300
TELEFAX: (617) 723-8923

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2179
TYPE: Nucleic acid
STRANDEDNESS: Double
TOPOLOGY: Linear
MOLECULE TYPE: cDNA to mRNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
TISSUE TYPE: Testis
IMMEDIATE SOURCE:
LIBRARY: Igt11 cDNA library, Clontech #HL1010b
CLONE: pHSR11-11, pHSR15-6
FEATURE:
NAME/KEY: protein coding region
LOCATION: 75 to 2159
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-08-474-986-1

Query Match
Best Local Similarity 47.3%; Pred. No. 3.1e-08;
Matches 192; Conservative 0; Mismatches 214; Indels 0; Gaps 0;

1166 ACTGCTCTATGCTCCCATGTCGGAATATGTAATGCTTGACGAGCGGATTTCTTCAT 1225
1081 ACTTATGCAATGAAAGTGTGACGTGACCTGCTCCCTTAAGCCAGATTCACACCCAT 1140

1226 TTGAGGACCTCTTGAGTAAATATCTCAGAAATATTTGTCTGGGTATAGCTTTCATTA 1285
1141 GTGAAGATATCAGGGGTACACATCTCTCAGAGTCCGATATGTTTATCAGATCTCTGG 1200

1286 CCTGCTTGGAAATCTTTTGTTCATTTGTCATGTCAGATGATCTTTCATTAAGCTGAAATACAA 1345
1201 CCATCACTGGGAACATCATAGTGTAGTATCTTAACCTACAGCAGCAATATAAATCAAG 1260

1346 CTACGCTATGTCATCAAAATCTTTGTTGTCGATGTCGTAATGCGGTATTAATCTTGT 1405
1261 TCCCCAGGTCCTTATGTGCACTGGGCTTGTGTGATCTCTGATTCGAAATCTACCTGC 1320

1406 TCTTTGTGGCAATTTTGCATATAAATACGAGGCGAGTATCAGAAATATGCTTGTCTGT 1465
1321 TGCTCATTTGATCATGTTGATATTCATACCAAGACCAATATACAACTAATGCCATTGACT 1380

1466 GGATGAGAGGTGCAATGCGGCTCATGAGGTTCTCGGCGATCTGTCCACGAAATCT 1525
1381 GGCAAACTGGGGCGAGGTGTGATGCTGCTGCTTTTTCATCTGTTTGGCAGTGAAGCTGT 1440

1526 CTGTTTGTGCTACTGACCTACTTGAATTTGAGAGAGTTCCGTGTCAT 1571
1441 CAGCTTCACTCTGACAGCTATCACTTGGAAAGATGGCATACCAT 1486

RESULT 6
US-09-016-434-1209
Sequence 1209, Application US/09016434
Patent No. 6500938

GENERAL INFORMATION:
APPLICANT: Janice Au-Young
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HERewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 845-4166
TELEFAX: (650) 845-0555
INFORMATION FOR SEQ ID NO: 1209:
SEQUENCE CHARACTERISTICS:
LENGTH: 2393 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: g182770
US-09-016-434-1209

Query Match
Best Local Similarity 47.3%; Pred. No. 3.3e-08;
Matches 192; Conservative 0; Mismatches 214; Indels 0; Gaps 0;

1166 ACTGCTCTATGCTCCCATGTCGGAATATGTAATGCTTGACGAGCGGATTTCTTCAT 1225
1073 ACTTATGCAATGAAAGTGTGACGTGACCTGCTCCCTTAAGCCAGATTCACACCCAT 1132

1226 TTGAGGACCTCTTGAGTAAATATCTCAGAAATATTTGTCTGGGTATAGCTTTCATTA 1285
1133 GTGAAGATATCAGGGGTACACATCTCTCAGAGTCCGATATGTTTATCAGATCTCTGG 1192

1286 CCTGCTTGGAAATCTTTTGTTCATTTGTCATGTCAGATGATCTTTCATTAAGCTGAAATACAA 1345
1193 CCATCACTGGGAACATCATAGTGTAGTATCTTAACCTACAGCAGCAATATAAATCAAG 1252

1346 CTACGCTATGTCATCAAAATCTTTGTTGTCGATGTCGTAATGCGGTATTAATCTTGT 1405
1253 TCCCCAGGTCCTTATGTGCACTGGGCTTGTGTGATCTCTGATTCGAAATCTACCTGC 1312

1406 TCTTTGTGGCAATTTTGCATATAAATACGAGGCGAGTATCAGAAATATGCTTGTCTGT 1465
1313 TGCTCATTTGATCATGTTGATATTCATACCAAGGCGCAATATACAACTAATGCCATTGACT 1372

QY 1466 GGATGAGAGCGTGCAGTCCGCCCTCATGGGGTTCCTGGCCATGCTGTCCACCGAAGTCT 1525
DB 1373 GGGAAATCTGGGGCAGAGCTGTGATGCTGCGCTTTTCACTGTCTTTGCGACGTAGCTGT 1432
QY 1526 CTGTCTCTACTAGTACCTTAATTGACTTTGGAGAAATGTTCTGTGCTAT 1571
DB 1433 CAGTCTACACTGTGACAGCTATACCTTGGAAAGATGCGATACCAT 1478

RESULT 7

US-09-016-434-1469
; Sequence 1469, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1469:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2413 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENEBANK
; CLONE: 9903759
; US-09-016-434-1469

Query Match 2.8%; Score 63; DB 4; Length 2413;

Best Local Similarity 47.6%; Pred. No. 5e-08;

Matches 186; Conservative 0; Mismatches 205; Indels 0; Gaps 0;

QY 1193 TATGTATGCGCTTGAAGGAGGCAATTTCTTCAATTGAGAGCACTTGGCTAACAAATATCC 1252
DB 1260 TGTGTACCCCAAGTCCGATGATTCACCCGTGTGAAGACATATAGGGCTACAAAGTTCC 1319
QY 1253 TCAGAAATTTTGTCTGGGTTAAGCTTTATTAACCTGCTTTGGAAATCTTTTGTGATTC 1312
DB 1330 TGAGAAATTTGTGTGGTTCGTTAGCTGCTGCTCTCTCGGCAATGCTTTGTCTGTC 1379
QY 1313 GCATAGATCTTTCATTAAAGCTGAATAATACATCAGCTATGTCCTCAAAATCTTT 1372
DB 1380 TTATCTCTCTACACAGCCACTACAAAGTACGTCCTCCGCTTTCTCATGTGCAACTGG 1439

QY 1373 GTTGTGATATTCCTATAGGAGGTTTACTTGTCTTTGTTGGCAATTTTCATATAAAT 1432
DB 1440 CCTTTGGGAAATTTTGATAGGGAGATACCTGCTCTCATGATGCTCTGTACACTTACA 1499
QY 1433 ACCGAGGCACTATACAGATATGCTTGTCTGTGATGAGAGGCTGACGTCCGCTCA 1492
DB 1500 CTCACCTGTGATCTACACCAACCATGCACTGAGCAGACAGGCCCTGGGTGCAACGCG 1559
QY 1493 TGGGATTCCTGGCCATGCTGTCCACCAAGTCTGTCTGTCTACTGACCTACTTGAATT 1552
DB 1560 CTGTTTCTTCACTGCTTTGCAAGCAGATTAATGATGATAGCTGACGATACACCC 1619
QY 1553 TGGAGAAATTCCTGTCATGTTCTTCCCTT 1583
DB 1620 TGAAGCGCTGTATGCCATACCTTCGCAAT 1650

RESULT 8

US-07-741-453A-62
; Sequence 62, Application US/07741453A
; Patent No. 6228597
; GENERAL INFORMATION:
; APPLICANT: PARMENTIER, MARC
; APPLICANT: LIBERT, FREDERIC
; APPLICANT: DUMONT, JACQUES
; APPLICANT: VASSART, GILBERT
; TITLE OF INVENTION: POLYPEPTIDES HAVING THYROTROPIN-RECEPTOR
; TITLE OF INVENTION: ACTIVITY NUCLEIC ACID SEQUENCES CODING FOR SUCH RECEPTORS
; TITLE OF INVENTION: AND POLYPEPTIDES, AND APPLICATIONS OF THESE POLYPEPTIDES
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN
; STREET: 1615 L STREET, N.W.
; CITY: WASHINGTON, D.C.
; COUNTRY: U.S.A.
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/741,453A
; FILING DATE: 19911015
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: KOKULIS, PAUL N.
; REGISTRATION NUMBER: 16773
; REFERENCE/DOCKET NUMBER: 91913/1107/US/ST
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3710 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-07-741-453A-62

Query Match 2.8%; Score 63; DB 3; Length 3710;

Best Local Similarity 47.6%; Pred. No. 6.5e-08;

Matches 186; Conservative 0; Mismatches 205; Indels 0; Gaps 0;

QY 1193 TATGTATGCGCTTGAAGGAGGCAATTTCTTCAATTGAGAGCACTTGGCTAACAAATATCC 1252
DB 1522 TGTGTACCCCAAGTCCGATGATTCACCCGTGTGAAGACATATAGGGCTACAAAGTTCC 1581
QY 1253 TCAGAAATTTTGTCTGGGTTTACTTTCATTACTGCTTTGGAAATCTTTTGTGATTC 1312

Db 1582 TGAGAAATGNGGTGGTTCGTTAGTCTGTGCTCTCTGAGCAATGCTTGTCTGTC 1641
Qy 1313 GCATGAGATCTTTGATTAAGCTGAAATACATCAAGTATGTCATCAAAATCTTT 1372
Db 1642 TTAATCTCTCACACACCATACAAAGTACGTCCTGCTTCTCATGTGCAACCTGG 1701
Qy 1373 GTTGTGCTGATTCCTGATGAGTGTGTTACTTGTCTTGTGTCATTTTGCATATTAAT 1432
Db 1702 CCTTGGGATTTCTGATGAGGATGATGCTGCTCTCATGCTCTGTAGACCTTACA 1761
Qy 1433 ACCGAGGAGATACAGAAATATGCTTGTCTGTGATGAGAGCGTGCAGTCCCTCA 1492
Db 1762 CTCACCTGAGTCTCAACCAATGCATCGATGAGACAGGCGCTGGGTGCAACAG 1821
Qy 1493 TGGGGTTCCTGGCAGCTGTCCACGAGTCTGTCTGTCTGCTACTGACCTTACTT 1552
Db 1822 CTGCTTCTTCACTGCTTGTGCAAGCATTAAGTGTATGAGCTGACGCTATCACCC 1881
Qy 1553 TGGAGAGTTCCTGTCATGCTTCCCTT 1583
Db 1882 TGAGAGCGCTGTATGCATCACCTTGGCAT 1912

RESULT 9

US-07-741-453A-57
; Sequence 57, Application US/07741453A
; Patent No. 6228597

GENERAL INFORMATION:

APPLICANT: PARMENTIER, MARC
APPLICANT: LIBERT, FREDERIC
APPLICANT: DUMONT, JACQUES
APPLICANT: VASARAT, GILBERT
TITLE OF INVENTION: POLYPEPTIDES HAVING THYROTROPIN-RECEPTOR
TITLE OF INVENTION: ACTIVITY, NUCLEIC ACID SEQUENCES CODING FOR SUCH RECEPTORS
AND POLYPEPTIDES, AND APPLICATIONS OF THESE POLYPEPTIDES
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DABRY & CUSHMAN
STREET: 1615 L STREET, N.W.
CITY: WASHINGTON, D.C.
COUNTRY: U.S.A.
ZIP: 20036

COMPUTER READABLE FORM:

MEDIUM TYPE: Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/741,453A
FILING DATE: 19911015
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16773
REFERENCE/DOCKET NUMBER: 91913/1107/US/ST
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714637 CUSH

INFORMATION FOR SEQ ID NO: 57:

SEQUENCE CHARACTERISTICS:
LENGTH: 4417 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-07-741-453A-57

Query Match

Best Local Similarity 47.6%; Score 63; DB 3; Length 4417;
Matches 186; Conservative 0; Mismatches 205; Indels 0; Gaps 0;

Qy 1193 TATGATGCCCTTGAAGCAGCATTTCTTCAATTGAGACCTCTTGCTAACAATATCC 1252

Db 1252 TGTGTACTCCTAAGTCAGATGATTCACACCCCTGGAAGACATTAATGGGCTACAGTTCC 1311
Qy 1253 TCAGAAATATTTCTCGGGTATAGCTTATTAATCACTGCTTTGGAATCTTTTTCATTTG 1312
Db 1312 TGAGATTTGTGTGTGTTTGTATGCTGTGCTCTCTCTGGAATGCTTTGTCTGGA 1371
Qy 1313 GCATGAGATCTTCTTAAGCTGAAATATACACTCAGCTATGTCATCAAAATCTTT 1372
Db 1372 TGTCTCTCTTACAGTCACTAATTAATGATCTGTCCACGCTTCTCATGTGCAACTTGG 1431
Qy 1373 GTTGTGCTGATTCCTGATGAGTGTGTTACTTGTCTTGTGTCATTTTGCATATTAAT 1432
Db 1432 CCTTGCAGATTTCTGATGAGGATGATCTGCTCTCATGCGCTCCGTAAGACCTTACA 1491
Qy 1433 ACCGAGGAGATACAGAAATATGCTTGTCTGTGATGAGAGCGTGCAGTCCGCTCA 1492
Db 1492 CTCATTTGAGTACTCAACCAATGCATCGATGAGACAGGCGCTGGGTATACAG 1551
Qy 1493 TGGGGTTCCTGGCAGCTGTCCACGAGTCTGTCTGTCTGCTACTGACCTTACTT 1552
Db 1552 CTGCTTCTTCACTGCTTGTGCAAGCATTAAGTGTATGAGCTGACGCTATCACCC 1611
Qy 1553 TGGAGAGTTCCTGTCATGCTTCCCTT 1583
Db 1612 TGAGAGCGCTGTATGCATCACCTTGGCAT 1642

RESULT 10

US-09-131-648-4
; Sequence 4, Application US/09131648
; Patent No. 6168920

GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Patterson, Chandra
TITLE OF INVENTION: EXTRACELLULAR ADHESIVE PROTEINS
FILE REFERENCE: PF-0576 US
CURRENT APPLICATION NUMBER: US/09/131,648
CURRENT FILING DATE: 1998-08-10
SOFTWARE: PERL Program
NUMBER OF SEQ ID NOS: 5
SEQ ID NO 4

LENGTH: 2290

TYPE: DNA
ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: 2687731

US-09-131-648-4

Query Match

Best Local Similarity 45.0%; Score 60.6; DB 3; Length 2290;
Matches 228; Conservative 0; Mismatches 279; Indels 0; Gaps 0;

Qy 425 TGTCTCTTAAGAAAACAAATCCACAGTCTTCAGATTAAGTTTTCATCAATACACAA 484
Db 424 TGTACTAGAGAAAACAACTTACTGAACTGCTGAAAATGTGTGCAACTGAGCA 483
Qy 485 AACTTAAAGATATTTCTTACGATTAATGCACTTGAACATATCCAGAAAACATTTT 544
Db 484 ACTTACAAGAACTTATTAATTAACAACTTGCTTTCTCAATTTCACTGAGCGCTTTA 543
Qy 545 TTGATTTATGTAATCGAAATATTAATCTCAACACACACAGTGCATACAACTCTAGAC 604
Db 544 TTGGCTTACATTAATCTTTCGACTTCATCTCAATTCAAATAGATTTGAGATATCAACA 603
Qy 605 CTGGAATATTTCAAGACTTACATCACTGCTTAATTTGATGATGACATCAATCAATAA 664
Db 604 GTAAAGTGTATTAAGCTCTTCCAAATCTAAGATTCGATGATGGGAAAATCAATTA 663
Qy 665 CCAAAATTTACAGCGCTGTATTAAGGATTAATTCCTTGTCTTCTGTCTATAGTTTA 724

Db 664 TCAGATGAAGAGACATGAACTTTAAGCCTCTTATCAATCTTCGACGCGCTGTTATAGCTG 723
Qy 725 ATAACTACTTGAAGAGCTCTTCCCAAGACAGATGTGCCCCAAATGCGCTCAACTCAACTGAG 784
Db 724 GTATTAACCTCAGCAAGAAATACCAAGATTAACGCTTGTTGAGACTGAAAACTTAGAAGCA 783
Qy 785 TGAATTTGAAAGGCAATGAATTAAGTATCTCAAAATTCACGTTTCTGTGCGCAT 844
Db 784 TCTCTTTTACGATTAACAGGCTTATTAAGTACCCCATGTTGCTCTTCAAAAAAGTTGTA 843
Qy 845 CGCTCAGAGTGTCTGTTCTGCTTAAATCAAAATGTTTGTTCAGAGAAAGCATTTT 904
Db 844 ATCTCAAAATTTTGGATCTAAATTAATAATCTTATTAATGAATACGAAGGGGTGATTTTA 903
Qy 905 CTTCAATTAATAATTTAGAGAACTGG 931
Db 904 GCAATATGCTACACTTAATAAGAGTTGG 930

RESULT 11
US-09-620-312D-350

; Sequence 350, Application US/09620312D

; Patent No. 6569662

; GENERAL INFORMATION:

; APPLICANT: Tang, Y. Tom

; APPLICANT: Liu, Chenghua

; APPLICANT: Asundi, Vinod

; APPLICANT: Zhang, Jie

; APPLICANT: Ren, Feiyun

; APPLICANT: Chen, Rui-hong

; APPLICANT: Zhao, Qing A.

; APPLICANT: Wehrman, Tom

; APPLICANT: Xue, Aidong J.

; APPLICANT: Yang, Yonghong

; APPLICANT: Wang, Jian-Rui

; APPLICANT: Zhou, Ping

; APPLICANT: Ma, Yundong

; APPLICANT: Wang, Dunrui

; APPLICANT: Wang, Zhiwei

; APPLICANT: John Tillinghast

; APPLICANT: Dmanac, Radote T

; TITLE OF INVENTION: No. 656962el Nucleic Acids and

; TITLE OF INVENTION: Polypeptides

; FILE REFERENCE: 784CIP2B

; CURRENT APPLICATION NUMBER: US/09/620,312D

; CURRENT FILING DATE: 2000-07-19

; PRIOR FILING DATE: 2000-04-25

; PRIOR APPLICATION NUMBER: 09/488,725

; PRIOR FILING DATE: 2000-01-21

; NUMBER OF SEQ ID NOS: 1105

; SOFTWARE: pc_Fl_genes Version 1.0

; SEQ ID NO 350

; LENGTH: 2461

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (232)..(2358)

; US-09-620-312D-350

Query Match 2.7%; Score 60.6; DB 4; Length 2461;

Best Local Similarity 45.0%; Pred. No. 2.5e-07;

Matches 228; Conservative 0; Mismatches 279; Indels 0; Gaps 0;

Qy 425 TGTCTTTAGAAAAAATCCACAGCTTCCAGATAAAGTTTTCATCAATACACA 484
Db 593 TGTACTAGAGAAAAAACAATCTACTGAACTGCTGAAAAAGTCTGCGAAGTGAACA 652
Qy 485 AACTTAAAAAGATATTTCTTCAAGATTAATGATTAAGACATATTCAGAGAAATTTT 544
Db 653 ACTTACAGAACTATATTAATTAACAACCTGTTCTTCAATTTCACTGAGAGCTTTA 712

Qy 545 TTGATTATGTATCTGCAATATTAATATCAACCAACTGACATCAACCTCAGAC 604
Db 713 TTGGCTACATATATCTTCTGATCTCATCTCAATTAATAATGATGATGATCAACA 772
Qy 605 CTGGAATATTTCAAGACTTACATCACTAAGTCTTATCTAGATGATCAATCAATTA 664
Db 773 GTAAAGTGTGAAGCTCTTCCAAATCTAGAGATTCGATGATGAGGAAAAATCAATTA 832
Qy 665 CCAGAAATTTCAAGAGGCTGTTTACGGGATTAATTCCTGTTTCTGCTGATGTTA 724
Db 833 TCAGAAATCAAGACATGAATCTTAAGCCTTTATCAATCTTCGACGCTGTTATAGCTG 892
Qy 725 ATAACTACTTGAAGAGCTCTTCCCAAGACAGATGTGCCCCAAATGCGCTCAACTCAACTGAG 784
Db 893 GTATTAACCTCAGCAAGAAATACCAAGATTAACGCTTGTTGAGACTGAAAACTTAGAAGCA 952
Qy 785 TGAATTTGAAAGGCAATGAATTAAGTATCTCAAAATTCACGTTTCTGTGCGCAT 844
Db 953 TCTCTTTTACGATTAACAGGCTTATTAAGTACCCCATGTTGCTTCAAAAAAGTTGTA 1012
Qy 845 CGCTCAGAGTGTCTGTTCTGCTTAAATCAAAATGTTTGTTCAGAGAAAGCATTTT 904
Db 1013 ATCTCAAAATTTTGGATCTAAATTAATAATCTTATTAATGAATACGAAGGGGTGATTTTA 1072
Qy 905 CTTCAATTAATAATTTAGAGAACTGG 931
Db 1073 GCAATATGCTACACTTAATAAGAGTTGG 1099

RESULT 12
US-08-985-335-4

; Sequence 4, Application US/08985335

; Patent No. 6080847

; GENERAL INFORMATION:

; APPLICANT: Hillman, Jennifer L.

; APPLICANT: Yve, Henry

; APPLICANT: Lal, Preeti

; APPLICANT: Shah, Purvi

; APPLICANT: Corley, Neil C.

; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL

; TITLE OF INVENTION: PROLIFERATION

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESS: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Dr.

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FASTSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/985,335

; FILING DATE: Filed Herewith

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Billings, Lucy J.

; REGISTRATION NUMBER: 36,749

; REFERENCE/DOCKET NUMBER: PF-0421 US

; TELEPHONE: 650-855-0555

; TELEFAX: 650-845-4166

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2082 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: LATRUT02
CLONE: 1352286
US-08-985-335-4

Query Match 2.6%; Score 57.8; DB 3; Length 2082;
Best Local Similarity 51.8%; Pred. No. 1.5e-06;
Matches 131; Conservative 0; Mismatches 122; Indels 0; Gaps 0;

QY 407 CTACATGTGACATTAAGTCTCTTAAAGAAAAACAATCCAGCTCTCCAGATTAAG 466
DB 505 CTCAGAGTTTGCGACATCTGCTAGCAAGAAAGATCCGACATTAAGAACACA 564
QY 467 TTTTCATCAATACACAACTTAAGAAAGATTTCTTCAGCATTAATGATTAAGACA 526
DB 565 TGTTCCTCAAGTTTAAAGAAAGCTGAAGCTGAGTGCAGAGAAAGATCTTAA 624
QY 527 TATCCAGAAAGATTTTGGATTATGATTAATCTGCAATATTAATCTCAACCAACT 586
DB 625 TTGAGAGTGAAGGCTTTGTTTAAACAACCTCAACCTCTTACGACACACACC 684
QY 587 GCATCAACACCTCAGACCTGGAATATTCAAAGCTTACATCAGCTAATGCTAATTC 646
DB 685 AGATCAAGCTTGAACGAGAAAGTGTTCATTTACACACCTCTTGAGCTACCTGCTC 744
QY 647 TAGATGACATCC 659
DB 745 TTTATGACAAACC 757

RESULT 13

US-09-410-372-4

Sequence 4, Application US/09410372
Patent No. 6281334
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
APPLICANT: Lal, Preeti
APPLICANT: Shah, Purni
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/410,372
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/985,335
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PP-0421 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 2082 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: LATRUT02
CLONE: 1352286
US-09-410-372-4

Query Match 2.6%; Score 57.8; DB 3; Length 2082;
Best Local Similarity 51.8%; Pred. No. 1.5e-06;
Matches 131; Conservative 0; Mismatches 122; Indels 0; Gaps 0;

QY 407 CTACATGTGACATTAAGTCTCTTAAAGAAAAACAATCCAGCTCTCCAGATTAAG 466
DB 505 CTCAGAGTTTGCGACATCTGCTAGCAAGAAAGATCCGACATTAAGAACACA 564
QY 467 TTTTCATCAATACACAACTTAAGAAAGATTTCTTCAGCATTAATGATTAAGACA 526
DB 565 TGTTCCTCAAGTTTAAAGAAAGCTGAAGCTGAGTGCAGAGAAAGATCTTAA 624
QY 527 TATCCAGAAAGATTTTGGATTATGATTAATCTGCAATATTAATCTCAACCAACT 586
DB 625 TTGAGAGTGAAGGCTTTGTTTAAACAACCTCAACCTCTTACGACACACACC 684
QY 587 GCATCAACACCTCAGACCTGGAATATTCAAAGCTTACATCAGCTAATGCTAATTC 646
DB 685 AGATCAAGCTTGAACGAGAAAGTGTTCATTTACACACCTCTTGAGCTACCTGCTC 744
QY 647 TAGATGACATCC 659
DB 745 TTTATGACAAACC 757

RESULT 14

US-07-157-342D-9

Sequence 9, Application US/07757342D
Patent No. 6218509
GENERAL INFORMATION:
APPLICANT: IGARASHI, Masao
APPLICANT: MINEGISHI, Takashi
APPLICANT: NAKAMURA, Kazuo
TITLE OF INVENTION: PROTEIN, DNA AND USE THEREOF
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN, DIKE, BRONSTEIN, ROBERTS &
CUSHMAN
STREET: 130 Water Street
CITY: Boston
STATE: Massachusetts
COUNTRY: US
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,342D
FILING DATE: 10-Sep-1991
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: BUCKLEY, Linda M.
REGISTRATION NUMBER: 31003
REFERENCE/DOCKET NUMBER: 41226
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
TELEFAX: (617)523-6440
TELEX: 200291 STRB UR
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 2022 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear


```

? MOLECULE TYPE: cDNA to mRNA
?
? FEATURE:
?
? NAME/KEY: CDS
? LOCATION: 1..2022
? SEQUENCE DESCRIPTION: SEQ ID NO: 9
US-07-757-342D-9

```

Query Match	2.5%	Score 57.6;	DB 3;	Length 2022;
Best Local Similarity	44.8%;	Pred. No. 1.7e-06;		
Matches 222; Conservative	0;	Mismatches 274;	Indels 0;	Gaps 0;

Qy	1081	GAAAGGATAGAGATCTCCAAATATAAACAAGATGTTCAACCATAGAAATCTTCT	1140
Db	838	GAAAGCAAGTATAGSAAAGTGAGTAAACAAACATTATTTCTTCATGCTGCTAGAGCT	897
Qy	1141	CACATTTATTTTCAAAAATTTCGATAGTCTCTATGCTCCCCATGTCGAATATGATG	1200
Db	898	GAACCTAGATGGCTGGGACTATAGAAATATGGTTTCTTACCCAGACACCCCGATGCTCT	957
Qy	1201	CCCTTGAAGGACGGGACTTTCTTCATTGAGGACCTCTTGGGCTAAACATATCCTGAAATA	1266
Db	958	CTGAGACCAAGATGCTTTTATATCCCTGTAGACATTATAGGGTATGALCTTCTTAGGGTC	1017
Qy	1261	TTTGTCTGGGTTATAGCTTTCACTTACCTGTCTTGGAAAATCTTTTGTCAITGGCATGAGA	1320
Db	1018	CTGATTTGGCTGATTAATATATTCTACCAATCAGGGAACATGACGTGTTCTTTTGTCTC	1077
Qy	1321	TCTTTCACTAAAGCTGAAATATCAACTCAAGTATGTCATCAAAATCCTTTGTTGTCCT	1380
Db	1078	CTGACAAAGCTGTATCAAACTTACAGTGCCTCGTTTCTCATATGCAATCTCTCTTTGGA	1133
Qy	1381	GATTGCTGATGGGTGTACTTGTCTTCTTTGTGGCAATTTTGCATATATAAATATACGAGGG	1440
Db	1138	GACTTTTGCAATGGGGCTCTATCTGTGCTCATAGCTCAGTTGATTTCCAAACCAAGGGC	1197
Qy	1441	CAGTATCAGAACTATAGCCTGTGCTGTGATGAGAGACGTGCAATGCGGCTCATAGGGGTTT	1500
Db	1198	CAGTACTATTAACCAATGACCATAGACTGCGACAGAGAGAGTGGGTGACGACTGCTGCTTT	1257
Qy	1501	CTGGCCATGCTGTCCACCGAAGCTCTCTGTTCTGTCACTACCACTTGAATTTGGAGAAG	1560
Db	1258	TTCACTGATTTGGCAAGTGAATTTCTGTCTACACCCCTCAGCGTATCACTGTAGAAAGA	1311
Qy	1561	TTCTCTGTCATTGTCTCT	1576
Db	1318	TGGCACACCATACCT	1333

RESULT 15
 US-07-757-342D-1
 ; Sequence 1, Application US/07757342D
 ; Patent No. 6218509
 ; GENERAL INFORMATION:
 APPLICANT: IGARASHI, Masao
 MINEGISHI, Takashi
 NAKAMURA, Kazuo
 TITLE OF INVENTION: PROTEIN, DNA AND USE THEREOF
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSSE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
 CUSHMAN
 STREET: 130 Water Street
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: US
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/757,342D

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1      FILING DATE: 10-Sep-1991
2      CLASSIFICATION: <Unknown>
3      ATTORNEY/AGENT INFORMATION:
4
5      NAME: BUCKLEY, Linda M.
6      REGISTRATION NUMBER: 31003
7      REFERENCE/DOCKET NUMBER: 41226
8      TELECOMMUNICATION INFORMATION:
9      TELEPHONE: (617) 523-3400
10     TELEFAX: (617) 523-6440
11     TELER: 200291 STRE UR
12
13     INFORMATION FOR SEQ ID NO: 1:
14
15     SEQUENCE CHARACTERISTICS:
16
17     LENGTH: 2987 base pairs
18     TYPE: nucleic acid
19     STRANDEDNESS: double
20
21     TOPOLOGY: linear
22
23     MOLECULE TYPE: cDNA to mRNA
24     FEATURE:
25
26     NAME/KEY: CDS
27     LOCATION: 1..2097
28
29     SEQUENCE DESCRIPTION: SEQ ID NO: 1:
30
31     US-07-757-342D-1

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Query Match	2.5%	Score 57.6	DB 3	Length 2987
Best Local Similarity	44.8%	Pred. No. 2	1e-06	
Matches	222	Conservative	0	Mismatches 274
			Indels	0
			Gaps	0
QY	1081	GAAGATAGAGATTCCTCAATATATAACAACAAGATGTTTCAACCCATGAGAAATCTTTC	1140	
DB	913	GAAGGACACGTAAAGAAAGTAGTAACAAACATTTATTTCTTCATGCTTGAGAGT	972	
QY	1141	CACATTTATTTCAAAAACTTTCGATCTGCTCCTATAGTCTCCCATATGCCAATATATATG	1200	
DB	973	GAAGTGAATGCTGGGACCTATGAATATATGTTCTTGCTTACCCAAAGACACCCGATGTC	1032	
QY	1201	CCCTTGAACGACGGCATTTCTTCATTTGAGGACCTCTTGCTAAACAATATCCTCAGAA	1260	
DB	1033	CCTGAACCAATGCTTTTAATCCTGTGAGAACATATATGGCTATGACTTCTTAAAGGTC	1092	
QY	1261	TTTGTCTGGGTTATAGCTTCATTACCTGCTTGGAAATCTTTTGTCAATGGCAGTGA	1320	
DB	1093	CTGATTTGGCTGATTAATATATCTAGCCATCATGGGAAACATGACGTGTTCTTTTGTCTC	1152	
QY	1321	TCTTTCAATTAAGCTGAAAAATACAATCACTGACCTATGTCATCAAAATCTTTGTGTGCT	1380	
DB	1153	CTGACAAATCGTTCAAACTACAGATGCTGCTGTTTCTCAATGTCAAATCTCTCTTGCA	1212	
QY	1381	GATGCGCTGATGGGNGTTACTTGTCTTGTGTTGGCATTTTCGATATATTAATACCGAGG	1440	
DB	1213	GACTTTTGCATGGGGCTTATCTGCTGCTCATAGCTCATGTTAATGCCAAACCAAGGCG	1272	
QY	1441	CAGATACGAAGTATGCCCTTGCCTGTGATGAGAGCGTGCAGTGCAGGCTCATGGGGTTC	1500	
DB	1273	CAGTACATTAACATGACCATAGACTGGGAGACAGGAGATGGGTGAGACATGCTGGCTT	1332	
QY	1501	CTGGCGATGCTGTCCACCGAAGTCTGTGTTGTGCTACTGACTTACTTGTGGAGAG	1560	
DB	1333	TTCACTGATATCGCAAGTAACTTGTGTCTACACCCCTCAACCTGATCATCTTAAAGAA	1392	
QY	1561	TTCCGTGATTTGTCT	1576	
DB	1393	TGGCACCAATCACT	1408	

Search completed: November 28, 2003, 19:19:49
Job time : 158 secs